

Result No.	Score	Query	Match	Length	DB ID	Description
1	2198	100.0	401	9	US-10-510-876-4	Sequence 4, Appli
2	2192	99.7	401	9	US-10-510-876-2	Sequence 2, Appli
3	2192	99.7	401	9	US-10-921-793-52	Sequence 52, Appli
4	2192	99.7	401	9	US-10-921-198-52	Sequence 52, Appli
5	2192	99.7	401	9	US-10-942-042-52	Sequence 52, Appli
6	2187	99.5	401	11	US-11-31-963-1	Sequence 1, Appli
7	2187	99.5	401	11	US-11-254-836-1	Sequence 1, Appli
8	2086	94.9	537	11	US-11-144-236-6	Sequence 6, Appli
9	2085	94.9	380	11	US-11-144-236-1	Sequence 1, Appli
10	1892	86.1	401	9	US-10-948-053-2	Sequence 2, Appli
11	1828	83.2	338	9	US-10-921-793-54	Sequence 54, Appli
12	1828	83.2	338	9	US-10-941-198-54	Sequence 54, Appli
13	1828	83.2	338	9	US-10-942-042-54	Sequence 54, Appli
14	1043	47.5	406	9	US-10-948-053-6	Sequence 6, Appli
15	1018	46.3	407	9	US-10-948-053-4	Sequence 3, Appli
16	1013.5	46.1	400	9	US-10-948-053-5	Sequence 4, Appli
17	1013.5	46.1	400	9	US-10-948-053-5	Sequence 5, Appli
18	1013	46.1	404	9	US-10-948-053-7	Sequence 7, Appli
19	1009	45.9	401	9	US-11-154-257-3	Sequence 8, Appli
20	945	43.0	161	11	US-11-042-814-8	Sequence 3, Appli
21	674	30.7	120	11	US-11-211-917-139	Sequence 8, Appli

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.8	Sequence 2, Appli
OM protein - protein search, using sw model	Sequence 16, Appli	Sequence 16, Appli
Run on: May 15, 2006, 19:21:20 ; Search time 16 Seconds (without alignments)	Sequence 6, Appli	Sequence 6, Appli
Title: US-09-718-725A-125	Sequence 4, Appli	Sequence 4, Appli
Perfect score: 2198	Sequence 2, Appli	Sequence 2, Appli
Sequence: 1 MNKILCCALVFLDISIKWT.....QKLFLEMIGNQVQSVKISCL 401	Sequence 2945, App	Sequence 2945, App
Scoring table: BLOSUM62	Sequence 5, Appli	Sequence 5, Appli
Gapext: 0.5	Sequence 32, Appli	Sequence 32, Appli
Searched: 250354 seqs, 46948837 residues	Sequence 32, Appli	Sequence 32, Appli
Total number of hits satisfying chosen parameters: 250354	Sequence 32, Appli	Sequence 32, Appli
Minimum DB seq length: 0	Sequence 32, Appli	Sequence 32, Appli
Maximum DB seq length: 2000000000	Sequence 32, Appli	Sequence 32, Appli
Post-processing: Minimum Match 0%	Sequence 32, Appli	Sequence 32, Appli
Maximum Match 100%	Sequence 32, Appli	Sequence 32, Appli
Listing first 45 summaries		

Database :	Published Applications AA_New;*	RESULT 1
	1: /SIDSS5_ptodata/1/pubpaa/US06_NEW_PUB.pep1:*	US-10-510-876-4
	2: /SIDSS5_ptodata/1/pubpaa/US06_NEW_PUB.pep1:*	; Sequence 4, Application US/10510876
	3: /SIDSS5_ptodata/1/pubpaa/US07_NEW_PUB.pep1:*	; Publication No. US2010000392841
	4: /SIDSS5_ptodata/1/pubpaa/US08_NEW_PUB.pep1:*	; GENERAL INFORMATION:
	5: /SIDSS5_ptodata/1/pubpaa/US08_PCT_NEW_PUB.pep1:*	; APPLICANT: Power, Christine
	6: /SIDSS5_ptodata/1/pubpaa/US09_NEW_PUB.pep1:*	; APPLICANT: Platner-Zyberk, Christine
	7: /SIDSS5_ptodata/1/pubpaa/US09_PCT_NEW_PUB.pep1:*	; TITLE OF INVENTION: Use of osteoprotegerin for the treatment and/or prevention of fi
	8: /SIDSS5_ptodata/1/pubpaa/US10_NEW_PUB.pep1:*	; FILE REFERENCE: SLII-P01-001
	9: /SIDSS5_ptodata/1/pubpaa/US10_PCT_NEW_PUB.pep1:*	; CURRENT APPLICATION NUMBER: US/10/510,876
	10: /SIDSS5_ptodata/1/pubpaa/US11_NEW_PUB.pep1:*	; CURRENT FILING DATE: 2004-10-08
	11: /SIDSS5_ptodata/1/pubpaa/US11_NEW_PUB.pep1:*	; PRIORITY NUMBER: EP02100364.5
	12: /SIDSS5_ptodata/1/pubpaa/US60_NEW_PUB.pep1:*	; PRIORITY FILING DATE: 2002-04-10
	Post. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	NUMBER OF SEQ ID NOS: 12
	SUMMARIES	SOFTWARE: PatentIn version 3.1
		SEQ ID NO: 4
		LENGTH: 401
		TYPE: PRT
		ORGANISM: Homo sapiens
		US-10-510-876-4

Query	Match	Score	DB 9:	Length	401;
Qy	1 MNKILCALVFLDISIKWTQETPPKLYHYDRETSQHLLCDKCPGPTYLKQHCTAKWT	100.0%;	Score 2198;	DB 9;	Best Local Similarity 100.0%; Pred. No. 6.4e-173;
	2 2192	99.7	100	0;	Matches 401; Mismatches 0; Gaps 0;
	3 2192	99.7	100	0;	
	4 2192	99.7	100	0;	
	5 2192	99.7	100	0;	
	6 2187	99.5	401	11	Db 1 MNKILCALVFLDISIKWTQETPPKLYHYDRETSQHLLCDKCPGPTYLKQHCTAKWT
	7 2187	99.5	401	11	Db 1 MNKILCALVFLDISIKWTQETPPKLYHYDRETSQHLLCDKCPGPTYLKQHCTAKWT
	8 2086	94.9	537	11	Qy 61 VCAPCPDHYYTDSWHTSDECCLYSPVCKELQVYKQBGNRTHANVCCEKGRYLEIEFCLK
	9 2085	94.9	380	11	Qy 61 VCAPCPDHYYTDSWHTSDECCLYSPVCKELQVYKQBGNRTHANVCCEKGRYLEIEFCLK
	10 1892	86.1	401	9	Db 61 VCAPCPDHYYTDSWHTSDECCLYSPVCKELQVYKQBGNRTHANVCCEKGRYLEIEFCLK
	11 1828	83.2	338	9	Qy 121 HRSCPDPFGVYQAGTPRNTVCKRCPGFFNETSSKAPCRKHTNSVFGLLTQKGNTA
	12 1828	83.2	338	9	Qy 121 HRSCPDPFGVYQAGTPRNTVCKRCPGFFNETSSKAPCRKHTNSVFGLLTQKGNTA
	13 1828	83.2	338	9	Qy 121 HRSCPDPFGVYQAGTPRNTVCKRCPGFFNETSSKAPCRKHTNSVFGLLTQKGNTA
	14 1043	47.5	406	9	Db 121 HRSCPDPFGVYQAGTPRNTVCKRCPGFFNETSSKAPCRKHTNSVFGLLTQKGNTA
	15 1018	46.3	407	9	Qy 120 Sequence 3, Appli
	16 1013.5	46.1	400	9	Sequence 4, Appli
	17 1013.5	46.1	400	9	Sequence 5, Appli
	18 1013	46.1	404	9	Sequence 54, Appli
	19 1009	45.9	401	9	Sequence 54, Appli
	20 945	43.0	161	11	Sequence 7, Appli
	21 674	30.7	120	11	Sequence 8, Appli

RESULT 2
 US-10-510-876-2
 ; Sequence 2, Application US/10510876
 ; Publication No US2006003928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Power, Christine
 ; APPLICANT: Plater-Zyberk, Christine
 ; TITLE OF INVENTION: Use of osteoprotogerin for the treatment and/or prevention of fib
 ; FILE REFERENCE: SU11-PA1-001
 ; CURRENT APPLICATION NUMBER: US/10/510,876
 ; CURRENT FILING DATE: 2004-10-08
 ; PRIOR APPLICATION NUMBER: EP02100364.5
 ; PRIOR FILING DATE: 2002-04-10
 ; NUMBER OF SEQ ID NOS: 12
 ; SEQ ID NO 2
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-510-876-2

Query Match 99.7%; Score 2192; DB 9; Length 401;
 Best Local Similarity 99.8%; Pred. No. 2e-172;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNKLCCALVPLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKHCTAKWKT 60
 Db 1 MNKLCCALVPLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECLYCSPYCKELQYKQECRHTNVCCKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYTDSWHTSDECLYCSPYCKELQYKQECRHTNVCCKEGRYLEIEFCLK 120
 Qy 121 HRSCPFGFVYQAGTPRNTVCKRCDGFSENNETSSKAPCRKHTHNSVFGLLLTQKGNT 180
 Db 121 HRSCPFGFVYQAGTPRNTVCKRCDGFSENNETSSKAPCRKHTHNSVFGLLLTQKGNT 180
 Qy 181 HDNICSNSESTOKCGIDVTLCEAFAFRFAVPTKTPNWLSVLVDNLPGTKVNAESVERI 240
 Db 181 HDNICSNSESTOKCGIDVTLCEAFAFRFAVPTKTPNWLSVLVDNLPGTKVNAESVERI 240
 Qy 241 KROHSSOEQTOLLKLUWKHONKAQDIVKKLQDILCENSYORHIGHANTTEFQLSIME 300
 Db 241 KROHSSOEQTOLLKLUWKHONKDQDVKCIQDILCENSYORHIGHANTTEFQLSIME 300
 Qy 301 SLPGKVGADIEKTIKACKPSDQIQLLSWIRKNGDQTLKGMLHALHSKTKTHFPKT 360
 Db 301 SLPGKVGADIEKTIKACKPSDQIQLLSWIRKNGDQTLKGMLHALHSKTKTHFPKT 360
 Qy 361 VTQSLKTTIRFLHSFTMVKLYQKFLFLEMIGNOVQSYKISCL 401
 Db 361 VTQSLKTTIRFLHSFTMVKLYQKFLFLEMIGNOVQSYKISCL 401

RESULT 4
 US-10-931-198-52
 ; Sequence 52, Application US/10931198
 ; Publication No. US20060045902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NYCZ, Jeffrey
 ; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
 ; FILE REFERENCE: 64118 000087
 ; CURRENT APPLICATION NUMBER: US/10/931,198
 ; CURRENT FILING DATE: 2004-09-01
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 52
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-931-198-52

Query Match 99.7%; Score 2192; DB 9; Length 401;
 Best Local Similarity 99.8%; Pred. No. 2e-172;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNKLCCALVPLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKHCTAKWKT 60
 Db 1 MNKLCCALVPLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECLYCSPYCKELQYKQECRHTNVCCKEGRYLEIEFCLK 120

Result No.	Score	Query Match	Length	DB ID	Description
1	2198	100.0	401	3	US-09-405-032-125 Sequence 125, App
2	2198	100.0	401	4	US-10-151-071-8 Sequence 8, Appli
3	2198	100.0	401	4	US-10-467-243-2 Sequence 2, Appli
4	2198	100.0	401	5	US-10-129-595-3 Sequence 3, Appli
5	2198	100.0	401	5	US-10-966-845-4 Sequence 4, Appli
6	2198	100.0	401	5	US-10-762-159-125 Sequence 125, App
7	2198	99.8	401	6	US-11-058-071-125 Sequence 125, App
8	2193	99.8	400	4	US-10-142-658-2 Sequence 2, Appli
9	2192	99.7	401	4	US-10-056-209-1 Sequence 1, Appli
10	2192	99.7	401	4	US-10-105-934-2 Sequence 2, Appli
11	2192	99.7	401	4	US-10-164-592-2 Sequence 2, Appli
12	2192	99.7	401	4	US-10-674-674-3 Sequence 3, Appli
13	2192	99.7	401	4	US-10-122-673-5 Sequence 5, Appli
14	2192	99.7	401	4	US-10-139-785-5 Sequence 5, Appli
15	2192	99.7	401	5	US-10-895-676-2 Sequence 2, Appli
16	2192	99.7	401	5	US-10-986-046-5 Sequence 5, Appli
17	2192	99.7	401	5	US-10-986-047-5 Sequence 5, Appli
18	2192	99.7	401	5	US-10-966-845-2 Sequence 2, Appli
19	2192	99.7	401	5	US-10-775-204-528 Sequence 528, App
20	2192	99.7	401	5	US-10-775-204-529 Sequence 529, App
21	2192	99.7	401	5	US-10-775-204-542 Sequence 542, App
22	2192	99.7	401	5	US-10-775-204-1238 Sequence 1238, App
23	2192	99.7	401	5	US-10-775-204-1239 Sequence 1239, App
24	2192	99.7	401	5	US-10-775-204-1240 Sequence 1240, App
25	2192	99.7	401	5	US-10-775-204-1241 Sequence 1241, App
26	2192	99.7	401	5	US-10-775-204-1242 Sequence 1242, App
27	2192	99.7	401	5	US-10-775-204-1243 Sequence 1243, App

RESULT 3
 US-10-467-243-2
 ; Sequence 2, Application US/10467243
 ; Publication No. US20040132971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maxygen Holdings Ltd.
 ; APPLICANT: Hauning, Jesper Mortensen
 ; APPLICANT: Hallier, Torben
 ; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
 ; FILE REFERENCE: 0226w0310
 ; CURRENT APPLICATION NUMBER: US/10/467,243
 ; CURRENT FILING DATE: 2003-08-06
 ; PRIORITY APPLICATION NUMBER: DK PA 2001 00214
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: US 60/267,843
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: DK PA 2001 00498
 ; PRIORITY FILING DATE: 2001-03-23
 ; PRIORITY APPLICATION NUMBER: US 60/278,320
 ; PRIORITY FILING DATE: 2001-03-23
 ; PRIORITY APPLICATION NUMBER: US 60/278,320
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-467-243-2

Query Match 100.0%; Score 2198; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175; Indels 0; Gaps 0
 Matches 401; Conservative 0; Mismatches 0;

Qy 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Db 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Qy 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Db 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Qy 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Db 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Qy 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Db 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Qy 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Db 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Qy 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Db 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Qy 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 Db 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 ; GENERAL INFORMATION:
 ; Sequence 3, Application US/10129595
 ; Publication No. US20050031583A1
 ; TITLE OF INVENTION: Uses of OPG Ligand to Modulate Immune Responses
 ; APPLICANT: Genentech, Inc. et al.
 ; CURRENT APPLICATION NUMBER: US/10/129,595
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/278,215
 ; PRIORITY FILING DATE: 2001-03-09

RESULT 2
 US-10-151-071-8
 ; Sequence 8, Application US/10151071
 ; Publication No. US20030017151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DOUGALL, William
 ; APPLICANT: ANDERSON, Dirk
 ; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
 ; FILE REFERENCE: 3277_A
 ; CURRENT APPLICATION NUMBER: US/10/151,071
 ; CURRENT FILING DATE: 2001-05-17
 ; PRIORITY APPLICATION NUMBER: 60/291,919
 ; PRIORITY FILING DATE: 2001-05-17
 ; SOFTWARE: Patent-in version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-151-071-8

Query Match 100.0%; Score 2198; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175; Indels 0; Gaps 0
 Matches 401; Conservative 0; Mismatches 0;

Qy 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Db 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Qy 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Db 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Qy 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Db 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Qy 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Db 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Qy 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 Db 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 ; GENERAL INFORMATION:
 ; Sequence 3, Application US/10129595
 ; Publication No. US20050031583A1
 ; TITLE OF INVENTION: Uses of OPG Ligand to Modulate Immune Responses
 ; APPLICANT: Genentech, Inc. et al.
 ; CURRENT APPLICATION NUMBER: US/10/129,595
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/278,215
 ; PRIORITY FILING DATE: 2001-03-09

RESULT 1
 US-10-129-595-3
 ; Sequence 3, Application US/10129595
 ; Publication No. US20050031583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc. et al.
 ; CURRENT APPLICATION NUMBER: US/10/129,595
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/278,215
 ; PRIORITY FILING DATE: 2001-03-09

Query Match 100.0%; Score 2198; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.3e-175; Indels 0; Gaps 0
 Matches 401; Conservative 0; Mismatches 0;

Qy 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Db 1 MNKLCCALVFLDISIKWTTQETPPKLYDEETSHQLLCDKCPGTYLKQHCTAKWKT 60
 Qy 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYTDSWHTSDECILYSPVCKELEYQVKECNRVCECKEGRYLEIEFCLK 120
 Qy 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Db 121 HRSCPDPGFGVYQAGTPRNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQGNAT 180
 Qy 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Db 181 HDN1SGNSB7OKC7IDVTLCEAFRFAVPTKTPNWISVLDNLPGTKVNAESVERI 240
 Qy 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Db 241 KROHSSQEBTQFLLWKHONKAQD1VKKTQDIDLCENSYQRHIGHANLTFEQLRSILME 300
 Qy 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 Db 301 SLPGKVKVGADELKETKACKPSDQ1LKLISWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
 ; GENERAL INFORMATION:
 ; Sequence 3, Application US/10129595
 ; Publication No. US20050031583A1
 ; TITLE OF INVENTION: Uses of OPG Ligand to Modulate Immune Responses
 ; APPLICANT: Genentech, Inc. et al.
 ; CURRENT APPLICATION NUMBER: US/10/129,595
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/278,215
 ; PRIORITY FILING DATE: 2001-03-09

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:59:30 ; Search time 28:3333 Seconds (without alignments)

1 MNKLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Title: US-09-718-725A-125

Perfect score: 2198

Sequence: 1 MNKLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /gn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /gn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /gn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /gn2_6/ptodata/1/iaa/PCT03_COMB.pep:*

5: /gn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /gn2_6/ptodata/1/iaa/baCfile81..pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2198	100.0	401	2 US-09-974-022-6	Sequence 6, Appli
2	2198	100.0	401	2 US-09-0422-785A-12	Sequence 12, Appli
3	2198	100.0	401	2 US-08-795-445A-6	Sequence 6, Appli
4	2198	100.0	401	2 US-08-974-186-6	Sequence 6, Appli
5	2198	100.0	401	2 US-08-974-186-6	Sequence 6, Appli
6	2198	100.0	401	2 US-08-795-445A-6	Sequence 6, Appli
7	2198	100.0	401	2 US-08-796-94D-128	Sequence 128, Appli
8	2198	100.0	401	2 US-08-577-788C-6	Sequence 6, Appli
9	2198	100.0	401	2 US-08-788C-56	Sequence 56, Appli
10	2198	100.0	401	2 US-09-054-832-2	Sequence 2, Appli
11	2192	99.7	401	2 US-09-153-922-1	Sequence 1, Appli
12	2192	99.7	401	2 US-09-072-993C-1	Sequence 1, Appli
13	2187	99.5	401	2 US-10-232-858-5	Sequence 5, Appli
14	2187	99.5	401	2 US-09-338-063A-5	Sequence 5, Appli
15	2177	99.0	401	2 US-10-232-858-62	Sequence 62, Appli
16	2177	99.0	401	2 US-10-232-858-63	Sequence 63, Appli
17	2177	99.0	401	2 US-10-332-858-64	Sequence 64, Appli
18	2177	99.0	401	2 US-10-232-858-65	Sequence 65, Appli
19	2177	99.0	401	2 US-10-232-858-66	Sequence 66, Appli
20	2177	99.0	401	2 US-09-338-063A-62	Sequence 62, Appli
21	2177	99.0	401	2 US-09-338-063A-63	Sequence 63, Appli
22	2177	99.0	401	2 US-09-338-063A-64	Sequence 64, Appli
23	2177	99.0	401	2 US-09-338-063A-65	Sequence 65, Appli
24	2177	99.0	401	2 US-09-338-063A-66	Sequence 66, Appli
25	2174	98.9	399	2 US-10-332-858-73	Sequence 73, Appli
26	2174	98.9	399	2 US-09-338-053A-73	Sequence 73, Appli
27	2174	97.4	393	2 US-10-232-858-67	Sequence 79, Appli

ALIGNMENTS

RESULT 1
US-09-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938

GENERAL INFORMATION:

; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Caldone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Agen Inc
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-6

Query Match 100.0% ; Score 2198; DB 2; Length 401;
Best Local Similarity 100.0% ; Pred. No. 1.7e-196;
Matches 401 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Qy 1 MNKLCCALVFLDISIKWTTOTFPKLYHYDEETSHQLLCDFKCPGFTYLKQHCTAKWKT 60
Db 1 MNKLCCALVFLDISIKWTTOTFPKLYHYDEETSHQLLCDFKCPGFTYLKQHCTAKWKT 60
Qy 61 VCAPPDHYTDSWMTSDECLYCSPVCKELQYVKQECNRTHNRCCEKBRYLETEBFCLK 120

RESULT 2
 i Sequence 12, Application US/09042785A
 i Patent No. 6194151
 i GENERAL INFORMATION:
 i APPLICANT: Bustield, Samantha J
 i TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 i TITLE OF INVENTION: AND USES THEREFOR
 i NUMBER OF SEQUENCES: 31
 i CORRESPONDENCE ADDRESS:
 i ADDRESS: LAHIVE & COCKFIELD, LLP
 i STREET: 28 State Street
 i CITY: Boston
 i STATE: Massachusetts
 i COUNTRY: USA
 i ZIP: 02109
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: PatentIn Release #1.0, Version #1.25
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/09/042,785A
 i FILING DATE: 17-MAR-1998
 i PRIOR APPLICATION DATA:
 i APPLICATION NUMBER: US 08/938,896
 i FILING DATE: 26-SEP-1997
 i ATTORNEY/AGENT INFORMATION:
 i NAME: Mandragores, Amy E
 i REGISTRATION NUMBER: 36,207
 i TELECOMMUNICATION INFORMATION:
 i TELEPHONE: (617)227-7400
 i TELEFAX: (617)742-4214
 i INFORMATION FOR SEQ ID NO: 12:
 i SEQUENCE CHARACTERISTICS:
 i LENGTH: 401 amino acids
 i TYPE: amino acid
 i TOPOLOGY: linear
 i MOLECULE TYPE: Peptide
 i FRAGMENT TYPE: internal
 i US-09-042-785A-12

RESULT 3
 i Sequence 6, Application US/08795445A
 i Patent No. 6284485
 i GENERAL INFORMATION:
 i APPLICANT: Boyle, William J.
 i APPLICANT: Lacey, David L.
 i APPLICANT: Calzone, Frank J.
 i APPLICANT: Chang, Ming-Shi
 i TITLE OF INVENTION: OSTEOPROTEGERIN
 i NUMBER OF SEQUENCES: 53
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: Amgen Inc.
 i STREET: 1840 Dehavenland Drive
 i CITY: Thousand Oaks
 i STATE: California
 i COUNTRY: USA
 i ZIP: 91320-1789
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: PatentIn Release #1.0, Version #1.30
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/08/795,445A
 i FILING DATE:
 i CLASSIFICATION:
 i PRIOR APPLICATION DATA:
 i APPLICATION NUMBER: 08/577,788
 i FILING DATE:
 i ATTORNEY/AGENT INFORMATION:
 i NAME: Winter, Robert B.
 i REFERENCE/DOCKET NUMBER: A-378
 i INFORMATION FOR SEQ ID NO: 6:
 i SEQUENCE CHARACTERISTICS:
 i LENGTH: 401 amino acids
 i TYPE: amino acid
 i TOPOLOGY: linear
 i MOLECULE TYPE: protein
 i MOLECULE TYPE: protein
 i US-08-795-445A-6

Query Match 100.0%; Score 2198; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.7e-196;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MNKLLCCALVFLDISIKWTQETFPKLYHYDEETSHOLLCDKCPGTYLKQHCTAKWKT 60

Query Match 100.0%; Score 2198; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.7e-196;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MNKLLCCALVFLDISIKWTQETFPKLYHYDEETSHOLLCDKCPGTYLKQHCTAKWKT 60

Scoring table:	BLOSUM62	Gapop 10.0	Gapext 0.5	Alignments
Searched:	2166443 seqs, 705528306 residues			
Total number of hits satisfying chosen parameters:	2166443			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0*			
	Maximum Match 100*			
Database :	UniProt_05_80:*			
	1: uniprot_sprot:*			
	2: uniprot_trembl:*			
Pred. No.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Match	Length	DB ID
1	219.2	99.7	401	1 TR11B_HUMAN
2	218.7	99.5	401	2 Q53TX6_HUMAN
3	190.6	86.7	401	1 TR11B_RAT
4	150.6	86.1	401	1 TR11B_MOUSE
5	159.8	72.7	402	2 Q48K2_CHICK
6	103.5	47.1	387	2 Q6GIN3_XENLA
7	61.3	27.9	146	2 Q72ZY4_CHICK
8	57.6	26.2	480	2 Q4SH87_TETNG
9	50.5	20.5	186	2 Q72ZY5_CHICK
10	44.4	20.2	300	1 TNR6B_HUMAN
11	41.1	18.7	302	2 Q9PNU0_SALFO
12	38.0	17.3	285	2 Q90W71_ONCMMY
13	37.2	16.9	285	2 Q9YQ66_ONCMMY
14	36.5	16.6	286	2 Q6NW61_BRARE
15	34.6	15.7	561	2 Q4SH86_tetradynio
16	34.5	15.7	637	2 Q5TYN2_BRARE
17	34.4	15.7	474	1 TNR1B_MOUSE
18	34.4	15.7	474	1 Q545P4_MOUSE
19	34.4	15.7	474	2 Q62327_MOUSE
20	34.3	15.6	459	2 Q6VAU8_RAT
21	33.3	15.2	461	2 TNR1B_RAT
22	33.3	15.2	474	1 Q5YLP0_RAT
23	33.3	15.2	474	1 TNR1B_HUMAN
24	33.0	15.0	461	1 Q5THJ5_HUMAN
25	33.0	15.0	461	2 Q9BSM6_CHICK
26	32.9	15.0	651	2 Q91ZM6_RAT
27	32.5	14.7	433	2 TNR21_HUMAN
28	30.2	13.8	655	1 Q800K7_PAROL
29	29.8	13.6	483	2 Q8IVS6_HUMAN
30	29.7	13.5	457	2 Q8IVB6_HUMAN
31	29.4	13.4	655	1 TNR21_MOUSE
32	294	13.4	655	2 Q543Y9_MOUSE
33	285	13.0	289	2 Q4QQW2_RATTUS_NORVIGIANUS
34	284.5	12.9	289	1 P27512_MOUSE
35	284.5	12.9	289	2 Q542B1_MOUSE
36	284.5	12.9	289	2 Q8K2X6_MOUSE
37	279.5	12.7	467	2 Q80010_CHICK
38	274.5	12.5	321	2 Q59EP9_HUMAN
39	270.0	12.3	169	2 Q9JKE0_RATTUS_NORVIGIANUS
40	269.5	12.3	625	1 Q35305_MOUSE
41	268	12.2	462	2 Q805b0_GALLUS_GALLUS
42	268	12.2	462	2 Q5ZL08_CHICK
43	268	12.2	463	2 Q4RZ8_TETNG
44	267.5	12.2	616	1 TNR11_HUMAN
45	267	12.1	278	2 Q85Q34_PIG

RESULT 1	TR11B_HUMAN	STANDARD;	PRT;	401 AA.
ID	TR11B_HUMAN			
AC	Q00300; Q60236; Q9UHP4;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DB	Tumor necrosis factor receptor superfamily member 11B precursor			
DE	(Osteoprotegerin) (Osteoclastogenesis inhibitory factor).			
GN	Name=INFRSF1B; Synonyms=OCIF, OGF;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RC	NUCLEOTIDE_SEQUENCE.			
RA	TISSUE=Kidney;			
RA	MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;			
RA	Simonet W.S., Lacey D.L., Dunsbar C.R., Kelley M., Chang M.-S., Luethey R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy B., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density"; Cell 189:309-319(1997).			
RT	"Osteoprotegerin: a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro"; Endocrinology 139:1329-1337(1998).			
RA	MEDLINE=98151033; PubMed=9492069; DOI=10.1210/en.139.3.1329; Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda B., Morinaga T., Higashio K.; "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro"; Endocrinology 139:1329-1337(1998).			
RA	RC	NUCLEOTIDE_SEQUENCE, AND VARIANT ASN-3.		
RA	TISSUE=Placenta;			
RA	MEDLINE=98351589; PubMed=9688283; Morinaga T., Nakagawa N., Yasuda H., Tsuda B., Higashio K., Higashio K.; "Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor"; Eur. J. Biochem. 254:685-691(1998).			
RA	RC	NUCLEOTIDE_SEQUENCE [GENOMIC DNA], AND VARIANT ASN-3 AND MET-104.		
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Shackwitz W.S., Sherwood J. K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; "NIH-SNPb, environmental genome project, NIBHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";			

Submitted (NOV-2003) to the EMBL/Genbank/DDbj databases.

[5] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA], AND VARIANT ASN-3.

RC TISSUE_EYE; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=988257; PubMed=1097932; DOI=10.1073/pnas.242603899;

RC STRAUBERG R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D., Klausner R.D., Zeiberg B., Buelow K., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullhy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Grimwood J., Garcia A.M., Gay L.J., Hulyk S.W., Villalain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Schein A., Jones J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98238645; PubMed=9571159; DOI=10.1006/bbrc.1998.8443;

RX RA Yamaoka A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H., Morigasa T., Tsuda E., Higashio K., "Characterization of monomeric and homodimeric forms of osteoclastogenesis inhibitor factor"; RT Biochem. Biophys. Res. Commun. 245:382-387 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX PubMed=15340161; DOI=10.1110/ps.04682504;

RX Zhang Z., Henzel W.J., "Signal peptide prediction based on analysis of experimentally verified cleavage sites"; RT Protein Sci. 13:2819-2824 (2004).

RX NUCLEOTIDE SEQUENCE OF 22-393.

RX TISSUE=Placenta; PubMed=1210935;

RX RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.; RT "Cloning and expression of osteoprotegerin from Homo sapiens.";

RX RY Acta Biolog. Biophys. Sin. 31:680-684 (1999).

RX PROTEIN SEQUENCE OF 242-255, 354-359 AND 369-378, AND FUNCTION.

RX MEDLINE=9712536; PubMed=9168977; DOI=10.1006/bbrc.1997.6603;

RX RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F., Morigasa T., Higashio K., "Isolation of a novel cytokine from human fibroblasts that specifically inhibits osteoclastogenesis"; RT Biochem. Biophys. Res. Commun. 234:137-142 (1997).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98269100; PubMed=5603945; DOI=10.1074/jbc.273.23.14363;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E., Morigasa T., Higashio K., "Characterization of structural domains of human osteoclastogenesis inhibitor factor.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

RX PROTEIN SEQUENCE OF 22-36 AND 378-401.

RX MEDLINE=98148056; PubMed=47894; DOI=10.1074/jbc.273.9.5117;

RX RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Dyn S., Silverman C., Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A., James J.E., Rosenberg M., Lee J.C., Young P.R.; RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

RX RY J. Biol. Chem. 273:5117-5123 (1998).

Copyright GenCore version 5.1.8
(c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:53:14 ; Search time 21 Seconds
(without alignment)
1837.282 Million cell updates/sec

Title: US-09-718-725A-125
Perfect score: 2198
Sequence: 1 MNKILCCALVFLDISKWT.....QKLEFLEMIGNQVQSVKISCL 401.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	15.7	474	B38634	tumor necrosis factor gene murine tumour necrosis factor receptor-6 - death receptor-6 - B cell-associated B-cell activation tumor necrosis factor gene G4R protein - G2R protein - vari T2 protein - rabb T2 protein - myxoma nerve growth factor FAS soluble protein nerve growth factor T-cell antigen 4-1 apoptosis-mediatin tumor necrosis fac nerve growth facto lymphocyte activat tumor necrosis fac
2	343	15.6	459	A33356	OX40 homolog - hum OX40 antigen precu tumor necrosis fac tumor necrosis fac CD30 antigen precu gene ox40 protein Fas antigen precu apoptosis-mediatin
3	330	15.0	461	D72175	
4	329	15.0	651	JCT705	
5	284.5	12.9	305	A46476	
6	264	12.0	277	A60771	
7	239.5	10.9	435	I54182	
8	232.7	10.8	348	T28623	
9	232.5	10.6	349	D36858	
10	229.5	10.4	349	A40036	
11	225	10.2	325	B43692	
12	219	10.0	326	1 GOVZML	
13	189.5	8.6	425	A26431	
14	189.5	8.6	314	I37383	
15	188.5	8.6	427	1 GOFTT1	
16	188	8.5	256	B32393	
17	186	8.4	461	1 GOFTT1	
18	185	8.4	335	JN0006	
19	177.5	8.1	416	I38426	
20	177	8.1	255	I38426	
21	176	8.0	454	1 GOFTT1	
22	174	7.9	277	I37552	
23	172	7.8	271	S12783	
24	168	7.6	455	1 GOFTT1	
25	168	7.6	461	JC4302	
26	158	7.2	595	2 A02086	
27	152.5	6.9	272	I48700	
28	152	6.9	324	JC2395	
29	140	6.4	327	A46484	

ALIGNMENTS

RESULT 1
B38634

tumor necrosis factor receptor type 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #Sequence_change 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: B38634; A40254; S5816

R:Lewis, M.; Tarraglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; PMID:1849278

A;Accession: B38634

A;Molecule type: mRNA

A;Residues: 1-474 <LEW>

A;Cross-references: UNIPARC:UPI0000003E93; GB:M60469; NID:9199827; PID:AAA39752.1; PID:R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine tumor necrosis factor A;Reference number: A40254; PMID:165445

A;Accession: A40254

A;Molecule type: mRNA

A;Residues: 1-474 <GOO>

A;Cross-references: UNIPARC:UPI0000003E93; ENBL:X07128; NID:9809043; PID:CAA60618.1; PID:R;Kissane, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.

Submitted to the EMBL Data Library, May 1995

A;Description: Characterization of the promoter region of the murine p75-TNF receptor.

A;Reference number: S54816

A;Accession: S54816

A;Cross-references: UNIPARC:UPI0000003E93; PID:9199827; PID:AAA39752.1; PID:R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor A;Reference number: A40254

A;Accession: A40254

A;Molecule type: mRNA

A;Residues: 1-22 <KLS>

C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); transmembrane protein

C;Keywords: cytokine receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-474/Domain: tumor necrosis factor receptor type 2 #status predicted <MAT>

F;40-77/Domain: NGF receptor repeat homology <NG1>

F;79-120/Domain: NGF receptor repeat homology <NG4>

F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match Score 344; DB 2; Length 474;

Best Local Similarity 33.3%; Pred. No. 4.8e-16;

Matches 83; Conservative 28; Mismatches 94; Gaps 9;

5 LCCALYFLDISIKWMTQETPPKYL-----HYDEETSHQLLCDKCPGP 47

6 LWWALVFE-LQQL-WATGHTVPAQVWLTQPKBEPGKBCQISQBYYDRKA-QMCCAKCPGP 61

48 TYLKQHCTAKRKTVCAPCPDHYYTDWSHTSDCECLCSPVCKBLQYKQBCNRTNRVYCEC 107

62 QYVKHFCNKTISDTVCADCEASMYTQWNQFRTCLSSESSSSCTDQEIRACTKQQRVYAC 121

108 KEGRMLIEF -----CLKHRSCLPPGFFGQGGTPERNTYCKRCPDGFPSNETSSKAPC 160

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model

Run on: May 15, 2006, 18:46:34 ; Search time 115.667 Seconds
(without alignments)

1523.264 Million cell updates/sec

Title: US-09-718-725A-125

Perfect score: 21.98

Sequence: 1 MNKLLC CALVFLDLSIKWTT.....QKLEPLEMIGNQVQSYKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378/81 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesed_21:*

1: genesedp19808:*

2: genesedp19908:*

3: genesedp20008:*

4: genesedp20018:*

5: genesedp20028:*

6: genesedp20038:*

7: genesedp20048:*

8: genesedp20058:*

9: genesedp20068:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

ARW38345 ID: AAW38345 standard; protein; 401 AA.

XX AC: AAW38345;

XX DT: 20-APR-1998 (first entry)

XX DE: Human osteoprotogerin.

XX KW: Osteoprotogerin; antibody; diagnosis; affinity purification; recombinant production; transgenic animal; treatment; prevention; antisense oligonucleotide; probe; detection; screening; human; bone disease; osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia.

XX OS: Homo sapiens.

XX PN: DE19654610-A1.

XX PD: 26-JUN-1997.

XX PF: 20-DEC-1996; 96DE-01054610.

XX PR: 22-DEC-1996; 95US-00577788.

XX PR: 03-SEP-1996; 96US-00706945.

XX (AMGEN INC.

XX PI: Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX DR: WPI: 1997-334271/31.

XX DR: N-PSDB; AATP063.

XX PT: Nucleic acid encoding osteoprotogerin - useful for treatment of diseases involving excessive bone loss, e.g. osteoporosis.

XX PS: Claim 23; Page 109-111; 182pp; German.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	21.98	100.0	401	2	AAW38345	Aaw38345 Human ost	
2	21.98	100.0	401	3	AAY43400	Aay43400 Osteoprot	
3	21.98	100.0	401	4	AAB66976	Aab66976 Human OPG	
4	21.98	100.0	401	5	ABG71823	Abg71823 Wild type	
5	21.98	100.0	401	6	ABP55109	Abp55109 Human ost	
6	21.98	100.0	401	6	AAC34363	Aac34363 Human ost	
7	21.98	100.0	401	7	ADD01627	Add01627 Human ost	
8	21.98	100.0	401	8	ADM28813	Adm28813 Human ost	
9	21.94	99.8	401	9	ABP19808	Abp19808 Osteoprot	
10	21.93	99.8	400	6	ABU08820	Abu08820 Human ost	
11	21.93	99.8	401	5	ABG73895	Abg73895 Human OPG	
12	21.93	99.8	401	5	ABG73894	Abg73894 Human OPG	
13	21.92	99.7	401	2	AAV05742	Aav05742 Tumour ne	
14	21.92	99.7	401	2	AAW95030	Aaw95030 Tumour ne	
15	21.92	99.7	401	2	AAW83926	Aaw83926 Human FTH	
16	21.92	99.7	401	3	AAB18715	Aab18715 A human t	
17	21.92	99.7	401	4	ABE60570	Ab60570 Human TNF	
18	21.92	99.7	401	5	ABG73893	Abg73893 Human OPG	
19	21.92	99.7	401	6	AAB36245	Aab36245 Human TRA	
20	21.92	99.7	401	6	AAC31135	Aac31135 Human TRA	
21	21.92	99.7	401	7	ADD01625	Add01625 Human ost	
22	21.92	99.7	401	7	ADP16158	Adp16158 Human alb	
23	21.92	99.7	401	7	ADP16153	Adp16153 Human alb	
24	21.92	99.7	401	7	ADP16151	Adp16151 Human alb	

CC cDNA libraries for related sequences. OPG can be used to treat or prevent
bone diseases, specifically excessive bone loss, e.g. osteoporosis,
CC Paget's disease, hypercalcemia, hyperparathyroidism, rheumatoid
arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
CC bone necrosis and osteopaenia

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2198; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.3e-161;
Matches 401; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MNKLCCALVLFDISIKWTTQETFPKLYDEETSHQLLDCKCPGTYLKQHCTAKWT 60

Db 1 MNKLCCALVLFDISIKWTTQETFPKLYDEETSHQLLDCKCPGTYLKQHCTAKWT 60

Db 1 HRS CPPGFVIVQAGTPRNTYCKRCPDGFFSNETSSKAPCRKHTNCSVFSLIITQGNAT 180

Db 121 HRS CPPGFVIVQAGTPRNTYCKRCPDGFFSNETSSKAPCRKHTNCSVFSLIITQGNAT 180

Qy 181 HDNICSNSSESTOKCGIDVTLCBAPFRPAPTKTPRNMITSVLDNLPGKVNAASSVERI 240

Db 181 HDNICSNSSESTOKCGIDVTLCBAPFRPAPTKTPRNMITSVLDNLPGKVNAASSVERI 240

Qy 241 KROHSSQEQTQFOLKLWKHQNAQDITVKKIQDIDCENSVQRHCHANLTFEQLRSME 300

Db 241 KROHSSQEQTQFOLKLWKHQNAQDITVKKIQDIDCENSVQRHCHANLTFEQLRSME 300

Qy 301 SLPGKVKVGAEDLEKTIKACKPSDQILKLUISLWRKINGDQDTLKGMLHKSCTYHFPKT 360

Db 301 SLPGKVKVGAEDLEKTIKACKPSDQILKLUISLWRKINGDQDTLKGMLHKSCTYHFPKT 360

Qy 361 VTQSLKKTTRFLHSETMYKLQKFLLEMIGNOVQSYKISCL 401

Db 361 VTQSLKKTTRFLHSETMYKLQKFLLEMIGNOVQSYKISCL 401

RESULT 2 AAB65976

ID AAY43400 standard; protein; 401 AA.

XX AC AAY43400;

DT 28-JAN-2000 (First entry)

XX DE Osteoprotegrin protein sequence.

XX KW Osteoprotegrin; OPG; human; cardiovascular disease; occlusion;

KW Monckeberg's arteriosclerosis; medial calcific sclerosis;

XX OS Homo sapiens.

XX PN WO9933942-A1.

XX PD 28-OCT-1999.

XX PP 21-APR-1999; 99WO-US008793.

XX PR 23-APR-1998; 98US-00064832.

XX PA (AMGB-) AMGEN INC.

XX PI Simonet S, Sarosi I;

XX DR WPI: 2000-013182/01.

DR N-PSDB; ARZ37254.

XX PT Treating and preventing cardiovascular diseases, especially

PT atherosclerosis and Monckeberg's arteriosclerosis.

XX Claim 9; Page 37-39; 43pp; English.

CC This sequence represents the human osteoprotegrin (OPG). The invention
CC relates to a method of treating or preventing cardiovascular disease by
CC administering OPG. The method can be used to treat and prevent
CC cardiovascular diseases associated with occlusion and calcification of
CC blood vessels, especially arteriosclerosis or Monckeberg's
CC arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
CC prevent cardiovascular diseases provides an alternative to invasive
CC treatments. OPG can be used as a single therapeutic for prevention and
CC treatment of both osteoporosis and cardiovascular diseases

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2198; DB 3; Length 401;

Best Local Similarity 100.0%; Pred. No. 3.3e-161;

Matches 401; Conservative 0; Mismatches 0; Gaps 0;

CC Indels 0; Gaps 0;

CC

XX PT atherosclerosis and Monckeberg's arteriosclerosis.

XX PS Claim 9; Page 37-39; 43pp; English.

XX XX

CC This sequence represents the human osteoprotegrin (OPG). The invention

CC relates to a method of treating or preventing cardiovascular disease by

CC administering OPG. The method can be used to treat and prevent

CC cardiovascular diseases associated with occlusion and calcification of

CC blood vessels, especially arteriosclerosis or Monckeberg's

CC arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or

CC prevent cardiovascular diseases provides an alternative to invasive

CC treatments. OPG can be used as a single therapeutic for prevention and

CC treatment of both osteoporosis and cardiovascular diseases

XX SQ Sequence 401 AA;

Query Match 100.0%; Score 2198; DB 3; Length 401;

Best Local Similarity 100.0%; Pred. No. 3.3e-161;

Matches 401; Conservative 0; Mismatches 0; Gaps 0;

CC Indels 0; Gaps 0;

CC

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 19:19:25 ; Search time 92 Seconds
 (without alignments)
 1821.191 Million cell updates/sec

Title: US-09-718-725A-123
 Perfect score: 2179
 Sequence: 1 MNKWLCCALLLIDIEWTT..... QKLFLEMIGNQVQSVKISCL 401
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1867569 seqs, 41/829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:
 1: /cgn2_6_ptodata/1/pubbaa/US07_PUBCOMB.pep*
 2: /cgn2_6_ptodata/1/pubbaa/US08_PUBCOMB.pep*
 3: /cgn2_6_ptodata/1/pubbaa/US09_PUBCOMB.pep*
 4: /cgn2_6_ptodata/1/pubbaa/US10_PUBCOMB.pep*
 5: /cgn2_6_ptodata/1/pubbaa/US10B_PUBCOMB.pep*
 6: /cgn2_6_ptodata/1/pubbaa/US11_PUBCOMB.pep*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2179	100.0	401	3	US-09-389-782-2	Sequence 2, Appli
2	2179	100.0	401	3	US-09-405-032-123	Sequence 123, Appli
3	2179	100.0	401	5	US-10-766-159-123	Sequence 123, Appli
4	2164	99.3	401	6	US-11-056-073-123	Sequence 123, Appli
5	2079	95.4	401	3	US-09-405-032-121	Sequence 121, Appli
6	2079	95.4	401	5	US-10-766-159-121	Sequence 121, Appli
7	2071	95.0	401	6	US-11-058-073-121	Sequence 121, Appli
8	2061	94.6	380	3	US-09-405-032-138	Sequence 138, Appli
9	2061	94.6	380	5	US-10-766-159-138	Sequence 138, Appli
10	2061	94.6	380	6	US-11-058-073-138	Sequence 175, Appli
11	1900	87.2	401	4	US-10-066-209-1	Sequence 1, Appli
12	1900	87.2	401	4	US-10-105-934-2	Sequence 2, Appli
13	1900	87.2	401	5	US-10-164-592-2	Sequence 2, Appli
14	1900	87.2	401	4	US-10-044-674-3	Sequence 3, Appli
15	1900	87.2	401	4	US-10-322-673-5	Sequence 5, Appli
16	1900	87.2	401	4	US-10-139-785-5	Sequence 5, Appli
17	1900	87.2	401	5	US-10-895-676-2	Sequence 2, Appli
18	1900	87.2	401	5	US-10-986-046-5	Sequence 5, Appli
19	1900	87.2	401	5	US-10-986-047-5	Sequence 5, Appli
20	1900	87.2	401	5	US-10-986-845-2	Sequence 2, Appli
21	1900	87.2	401	5	US-10-775-204-528	Sequence 528, Appli
22	1900	87.2	401	5	US-10-775-204-529	Sequence 529, Appli
23	1900	87.2	401	5	US-10-775-204-542	Sequence 542, Appli
24	1900	87.2	401	5	US-10-775-204-1238	Sequence 1238, Appli
25	1900	87.2	401	5	US-10-775-204-1239	Sequence 1239, Appli
26	1900	87.2	401	5	US-10-775-204-1240	Sequence 1240, Appli
27	1900	87.2	401	5	US-10-775-204-1241	Sequence 1241, Appli

ALIGNMENTS

RESULT 1
 US-09-389-782-2
 ; Sequence 2, Application US/09389782
 ; Publication No. US20030144187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wooden, Scott K.
 ; APPLICANT: Dunstan, Colin R.
 ; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
 ; FILE REFERENCE: A-604
 ; CURRENT APPLICATION NUMBER: US/09/389,782
 ; CURRENT FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 50
 ; SEQ ID NO: 2
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-389-782-2

Query	Match	Best Local Similarity	100.0% ; Score 2179;	DB 3 ; Length 401;
Matches	401 ;	Conservative	100.0% ; Pred. No. 4.4e-171;	Matches 0 ; Indels 0 ; Gaps 0 ;
Qy	1	MNKWLCCALLVLDIIEWTWTQTLPPKLYADPTEGHOLLCDKCAPTYLKOHCTVTKT	60	
Db	1	MNKWLCCALLVLDIIEWTWTQTLPPKLYADPTEGHOLLCDKCAPTYLKOHCTVTKT	60	
Qy	61	LCVPCPDHSYTDWSWHTSDECYCSPICKELOSVKQECNRTRHVRVCEBGRYLTIEFLK	61	
Db	61	LCVPCPDHSYTDWSWHTSDECYCSPICKELOSVKQECNRTRHVRVCEBGRYLTIEFLK	61	
Qy	61	HRSCPPGSGIVYQAGTPPERNTYCKKCPDGFSSGETSSKAPCTKHTNCSTFGLLIQLQKNTA	180	
Db	121	HRSCPPGSGIVYQAGTPPERNTYCKKCPDGFSSGETSSKAPCTKHTNCSTFGLLIQLQKNTA	120	
Qy	61	KRRHSSDQEQTOLLKWHQRDQENYTKC1QDIDUCESYQRHLHSNLTTEQJLALME	300	
Db	241	KRRHSSDQEQTOLLKWHQRDQENYTKC1QDIDUCESYQRHLHSNLTTEQJLALME	300	
Qy	301	SLPGKKSUSPEELERTKCKSSEQLLKLISLWRKNGDQPTLKALYALKLTKTSHPKT	360	
Db	301	SLPGKKSUSPEELERTKCKSSEQLLKLISLWRKNGDQPTLKALYALKLTKTSHPKT	360	
Qy	361	VTHSLRKTMRFLHFSPTMFLYRLYQKLFLPEMIGNQVQSYKISCL	401	

Db 361 VTHSLRKTMRFLLHSFTMRYQLFLMIGNOVQSVKISCL 401

RESULT 2

US-09-405-032-123

Sequence 123, Application US/09405032

Publication No. US201030207827A1

GENERAL INFORMATION:

APPLICANT: Amgen Inc.

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEES: Amgen Inc.

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

ZIP: 91320

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/405,032

FILING DATE: 24-Sep-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378-CIP2

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 123:

us-09-405-032-123

Query Match 100.0%; Score 2179; DB 3; Length 401;

Best Local Similarity 100.0%; Pred. No. 4.4e-171;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIENTTQETLPPKLYHDPETGHQLLCDKCAPTYLQHCTYRKRT 60

Db 1 MNKWLCCALLVLDIENTTQETLPPKLYHDPETGHQLLCDKCAPTYLQHCTYRKRT 60

Qy 61 LCVPCPDHSYDTSWHTSDECYCSPVCKELQSVKQECNRTHNRCBEGRYLEIEFCLK 120

Db 61 LCVPCPDHSYDTSWHTSDECYCSPVCKELQSVKQECNRTHNRCBEGRYLEIEFCLK 120

Qy 61 LCVPCPDHSYDTSWHTSDECYCSPVCKELQSVKQECNRTHNRCBEGRYLEIEFCLK 120

Db 61 LCVPCPDHSYDTSWHTSDECYCSPVCKELQSVKQECNRTHNRCBEGRYLEIEFCLK 120

Qy 121 HRSCPQPGSVVQAGTPERNNTYCKCPDGFFSGETTSKAPC1KHTNCSTFGILLIOKGNAT 180

Db 121 HRSCPQPGSVVQAGTPERNNTYCKCPDGFFSGETTSKAPC1KHTNCSTFGILLIOKGNAT 180

Qy 181 HDNVCSGNREATOKCGIDVTCBAAFPAPVTKIIPWLSVLDLSLPGTKNAESVERI 240

Db 181 HDNVCSGNREATOKCGIDVTCBAAFPAPVTKIIPWLSVLDLSLPGTKNAESVERI 240

Qy 241 KRRHSSQFTQQLKWHQNRDQEMYKIIQDIDCCESSVORHLGHSNLTQOLLALME 300

Db 241 KRRHSSQFTQQLKWHQNRDQEMYKIIQDIDCCESSVORHLGHSNLTQOLLALMB 300

Qy 301 SLPGKKISPEETERTRKCKSSQQLKLSWRIKNGQDQDTLKGMLYALKHLTKTSHPKT 360

Db 301 SLPGKKISPEETERTRKCKSSQQLKLSWRIKNGQDQDTLKGMLYALKHLTKTSHPKT 360

Qy 361 VTHSLRKTMRFLLHSFTMRYQLFLMIGNOVQSVKISCL 401

Db 361 VTHSLRKTMRFLLHSFTMRYQLFLMIGNOVQSVKISCL 401

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 18:59:30 ; Search time 28.3333 Seconds
(without alignments)

1170.104 Million cell updates/sec

Title: US-09-718-725A-123

Perfect score: 21.9

Sequence: 1 MNKWLCCALLVLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext: 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6.ptodata/1/iaa/5.COMB.pep:*

2: /cgn2_6.ptodata/1/iaa/6.COMB.pep:*

3: /cgn2_6.ptodata/1/iaa/H.COMB.pep:*

4: /cgn2_6.ptodata/1/iaa/PECTNS.COMB.pep:*

5: /cgn2_6.ptodata/1/iaa/RE.COMB.pep:*

6: /cgn2_6.ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	21.79	100.0	401	US-08-974-022-4
2	21.79	100.0	401	US-09-042-785A-13
3	21.79	100.0	401	US-08-795-445A-4
4	21.79	100.0	401	US-08-795-447A-4
5	21.79	100.0	401	US-08-974-186-4
6	21.79	100.0	401	US-08-795-446B-4
7	21.79	100.0	401	US-08-706-945D-126
8	21.79	100.0	401	US-08-577-788C-4
9	21.79	100.0	401	US-08-577-788C-54
10	20.79	95.4	401	US-08-974-022-2
11	20.79	95.4	401	US-08-795-445A-2
12	20.79	95.4	401	US-08-795-446A-2
13	20.79	95.4	401	US-08-974-186-2
14	20.79	95.4	401	US-08-795-446B-2
15	20.79	95.4	401	US-08-706-945D-124
16	20.79	95.4	401	US-08-577-788C-2
17	20.79	95.4	401	US-08-577-788C-55
18	19.95	89.7	364	US-08-706-945D-141
19	19.90	87.2	401	US-09-152-927-1
20	19.90	87.2	401	US-09-072-993C-1
21	18.95	87.0	401	US-10-232-858-52
22	18.95	87.0	401	US-09-333-063A-5
23	18.92	86.8	401	US-08-974-022-6
24	18.92	86.8	401	US-09-042-785A-12
25	18.92	86.8	401	US-08-795-445A-6
26	18.92	86.8	401	US-08-795-447A-6
27	18.92	86.8	401	US-08-974-186-6

ALIGMENTS

RESULT 1
US-08-974-022-4
; Sequence 4, Application US/08974022
; Patent No. 601538

GENERAL INFORMATION:

; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc
; STREET: 1840 Dehaviland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974, 022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; REFERENCE: Winter, Robert B.
; DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-974-022-4

Query Match Score 2179; DB 2; Length 401;
Best Local Similarity 10.0%; Pred. No. 3.4e-195;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHDPETGQHQLCDKCAPSTYLKQHCTVRK 60

Qy 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHDPETGQHQLCDKCAPSTYLKQHCTVRK 60

Db 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHDPETGQHQLCDKCAPSTYLKQHCTVRK 60

Qy 61 LCVCPDPHSYDTSWHTSDECYCSPPCKELQSVKQBCNRTHRNVCBEGRYLEIEFLCK 120

RESULT 2

Sequence 13, Application US/09042785A

Patent No. 6,194,151

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J

TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,785A

FILING DATE: 17-MAR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/938,896

FILING DATE: 26-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy E

REGISTRATION NUMBER: 36,207

REFERENCE DOCKET NUMBER: MEI-001CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

FRAGMENT TYPE: internal

US-09-042-785A-13

Query Match 100.0%; Score 2179; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 3.4e-195;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MNKWLCCALLVLDIEMTTOETLPPKLYHDPETGHQLLCDKCAPGTYLKOHCTVRRKT 60

Db 61 LCVPCPDHSYTSWHTSBVYCSPVCKRLQSVKQBCNTRINVCCEGRTLEIFCCLK 120

Qy 121 HRSCPPGGVVQAGTPENTVCKKCPDFFGETSSAKPCIGTNCSTFGILLIQGNAT 180

Db 121 HRSCPPGGVVQAGTPENTVCKKCPDFFGETSSAKPCIGTNCSTFGILLIQGNAT 180

Qy 181 HDNVC5GRREATOKCGIDVTLCBAAFPAPTKIIPNWLSLVDLPGTKVNAESVERI 240

Db 181 HDNVC5GRREATOKCGIDVTLCBAAFPAPTKIIPNWLSLVDLPGTKVNAESVERI 240

Qy 241 KRRHSSQEQTQFQKLWKRHQRDQEMYKIIQDIDCCESSYORHLGHSLNTEQQLALME 300

Db 241 KRRHSSQEQTQFQKLWKRHQRDQEMYKIIQDIDCCESSYORHLGHSLNTEQQLALME 300

Qy 301 SLPGKKSPEELERTRKCKSSQQLKLSWRIKNGDQTLKGMLYALKLKTSHPPKT 360

Db 301 SLPGKKSPEELERTRKCKSSQQLKLSWRIKNGDQTLKGMLYALKLKTSHPPKT 360

Qy 361 VTHSLRKTMRFLHSFTMRYLQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMRYLQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMRYLQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMRYLQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMRYLQKLFLEMIGNQVQSVKISCL 401

RESULT 3

US-08-795-445A-4

Sequence 4, Application US/08795445A

Patent No. 6,284,485

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,445A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-795-445A-4

Query Match 100.0%; Score 2179; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 3.4e-195;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MNKWLCCALLVLDIEMTTOETLPPKLYHDPETGHQLLCDKCAPGTYLKOHCTVRRKT 60

CC	blocks the inhibition of osteoclastogenesis.	FT	VARIANT	296	296	L -> R (in strain 129/Ola and strain NIH Swiss).
CC	-I- Homicidem.	FT	SEQUENCE	401 AA:	45923 MW;	CAB6102D3B312470 CRC64;
CC	-I- SUBCELLULAR LOCATION: Secreted	Query Match	100.0%	Score 2179;	DB 1;	Length 401;
CC	-I- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta, and in embryo.	Best Local Similarity	100.0%	Pred. No. 1.	6e-142;	Indels 0; Gaps 0;
CC	-I- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.	Matches 401;	Conservative 0;	MS matches 0;		
CC	-I- INDUCTION: Up-regulated by TGF-beta and estrogens. Down-regulated by 1,25-dihydroxyvitamin D3 and parathyroid hormone.	QY	1	MNKWLCALLVLDLIEWTTOETLPKLYHYDPIETGHQJLCDKCAPGTYLKQHCTVRRKT 60		
CC	-I- SIMILARITY: Contains 2 death domains.	Db	1	MNKWLCALLVLDLIEWTTOETLPKLYHYDPIETGHQJLCDKCAPGTYLKQHCTVRRKT 60		
CC	-I- SIMILARITY: Contains 4 TNFR-Cys repeats.	Qy	61	LCVPCPDHSYTDMSHTSDECYCSPICKELOSVKQECBNCNTRHNRVCEBEGRYLEBFCLK 120		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	Db	61	LCVPCPDHSYTDMSHTSDECYCSPICKELOSVKQECBNCNTRHNRVCEBEGRYLEBFCLK 120		
CC	DR EMBL: AB03311; ARB:G3108.1; -; mRNA.	Qy	61	HRSCPQSGVYQAGTPERNTVCKCPDGFRRGETSSKAPC1KHTNCSTFGILLIQKGNT 180		
CC	DR EMBL: AB013898; BAA20269.1; -; mRNA.	Qy	121	HRSCPQSGVYQAGTPERNTVCKCPDGFRRGETSSKAPC1KHTNCSTFGILLIQKGNT 180		
CC	DR EMBL: AB013903; BAA33388.1; -; Genomic DNA.	Db	121	HRSCPQSGVYQAGTPERNTVCKCPDGFSSGETSSKAPC1KHTNCSTFGILLIQKGNT 180		
CC	DR HSSP; O14763; 1DG.	Qy	181	HDNVCSGNREATQKGIDVTLCEBAEFFRFAVPTKLIIPNWLPSVLPGTKVNAESVERI 240		
CC	DR Ensemble: ENSMUSG00000063727; Mus musculus.	Db	181	HDNVCSGNREATQKGIDVTLCEBAEFFRFAVPTKLIIPNWLPSVLPGTKVNAESVERI 240		
DR	MGI: MGI:109587; Thrsf11b.	Qy	241	KRRHSSQEQTPOLLKWLKHQNRDQMVKKLQDIDCCESSVQRHGHSNLTTEQJALME 300		
DR	GO: GO:000578; C:extracellular matrix (sensu Metazoa); IDA.	Db	241	KRRHSSQEQTPOLLKWLKHQNRDQMVKKLQDIDCCESSVQRHGHSNLTTEQJALME 300		
DR	GO: GO:0005615; C:extracellular space; TAS.	Qy	301	SLPGKKSQPEEIERTRKTCGSBQLKLLSIWRKNGDQTLKGMYALKHKTSHFPKT 360		
DR	GO: GO:0042489; P:negative regulation of odontogenesis (sensu . . .); IDA.	Db	301	SLPGKKSQPEEIERTRKTCGSBQLKLLSIWRKNGDQTLKGMYALKHKTSHFPKT 360		
DR	Interpro: IPR000448; Death.	Qy	361	VTHSLRKTMRFHSFTMRYLQKLFILEMIGNOVQSYKISCL 401		
DR	Interpro: IPR010129; DEATH-like.	Db	361	VTHSLRKTMRFHSFTMRYLQKLFILEMIGNOVQSYKISCL 401		
PFam; PF000531; Death; 1.	PFam; PF000020; TNFR_c6; 3.					
SMART; SM00005; DEATH_1.	SMART; SM00208; TNFR_c6; 3.					
DR	PROSITE: PS50017; DEATH DOMAIN; 1.					
DR	PROSITE: PS000652; TNFR_NGPR_1; 1.					
KW	Apoptosis; Glycoprotein; Polymorphism; Receptor; Repeat; Signal.					
FT	SIGNAL 1 21					
CHAIN	22 401					
FT						
REPEAT	24 62					
FT	REPEAT 65 105					
FT	REPEAT 107 142					
FT	REPEAT 145 185					
FT	DOMAIN 198 269					
FT	DOMAIN 283 365					
FT	SITE 400 400					
FT	CARBODY 98 98					
FT	CARBODY 165 165					
FT	CARBODY 178 178					
FT	CARBODY 289 289					
FT	DISULFD 41 54					
FT	DISULFD 44 62					
FT	DISULFD 65 80					
FT	DISULFD 83 97					
FT	DISULFD 87 105					
FT	DISULFD 107 118					
FT	DISULFD 124 142					
FT	DISULFD 145 160					
FT	DISULFD 166 185					
FT	VARIANT 138 138					
FT	VARIANT 161 161					
FT	VARIANT 165 165					
FT	VARIANT 288 288					

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model

Run on: May 15, 2006, 18:53:14 ; Search time 21 Seconds
 (without alignments)
 1837.282 Million cell updates/sec

Title: US-09-718-725A-123
 Perfect score: 2.79

Sequence: 1 MNKWLCCALLLIDIEWTT..... QKLFLEMIGNQVQSVKISCL 401.

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_90.4
 1: pIR1;*
 2: pIR2;*
 3: pIR3;*
 4: pIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	314	14.4	459	2	I48854	gene murine tumour
2	312	14.3	461	1	B38536	tumor necrosis fac
3	312	14.3	474	2	B38634	tumor necrosis fac
4	300.5	13.8	651	2	JC7705	death receptor-6 -
5	270	12.4	305	2	A46416	B cell-associated
6	261	12.0	277	2	A60771	B-cell activation
7	244	11.2	435	2	I54182	tumor necrosis fac
8	233.5	10.7	325	1	A24632	T2 protein - rabbit
9	220	10.1	326	1	GOVZNL	T2 protein - myxom
10	217	10.0	349	2	D36858	gene GR protein -
11	216	9.9	349	2	D72175	G2R protein - vari
12	215.5	9.9	348	2	T28823	hypothetical prote
13	199	9.1	427	1	QH0H	nerve growth facto
14	197.5	9.1	425	1	A26431	nerve growth facto
15	184	8.4	416	1	JN0006	apo
16	182	8.4	335	2	A40036	apo
17	175.5	8.2	314	2	B37383	apo
18	177	8.1	256	2	B3293	T-cell antigen 4-1
19	167	7.7	255	2	I38926	lymphocyte activat
20	165.5	7.6	461	2	JC4302	tumor necrosis fac
21	163	7.5	271	2	S12783	OX40 antigen precu
22	161.5	7.4	454	1	Q0M571	tumor necrosis fac
23	160	7.3	455	1	GQHDT1	tumor necrosis fac
24	153	7.0	461	1	GQRT1	gene ox40 protein
25	152.5	7.0	272	2	I48700	OX40 homolog - hum
26	151	6.9	277	2	I37552	Fas antigen precu
27	149.5	6.8	324	2	JC2395	apo
28	143	6.6	327	2	A46384	apo
29	142.5	6.5	2823	2	F87908	protein T2A3.8 [i]

RESULT 1

I48854

Gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48854

R. Powell, E. E.; Wicker, L. S.; Peterson, L. B.; Todd, J. A.

Mamm. Genome 5, 726-727, 1994

A>Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A:Reference number: I48854 ; MUID: 95178848 ; PMID: 7873884

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-459 <RES>

A:Cross-references: UNIPROT:Q62327; UNIPARC:UPI00000E7DB6; EMBL:X76401; NID:9433830; PI

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2) ; NGF receptor repeat homology <NGF> F:151-188/Domain: NGF receptor repeat homology <NGF>

Query	Match	Score	Length	459;
Qy	18 WTTQETLPPKYL-LHYDPETGH-----QLICDKCAGPTYLKQHCTVRRKTL	34.61;	DB	26;
Qy	2 WATGHTYPAQVYLTPKPEPGYECQIQSQEYTYDRAKQMCCKCPTQVKTSDPTVC	34.61;	DB	20; Mismatches 79; Indels 26; Gaps 4;
Qy	63 VPCDPDHSYTDWSIHTSDECVYCPVCKLQSVKQBNCRTHNRYCCEGRYLBIBF-----	11.7	DB	66; Conservative 34.61;
Qy	62 ADCEASNYTQWQNQFRLCQLSSSSCSTDQVETRACTPKQONRVCAEGRYCAALKTHSGSC	12.1	DB	66; Best Local Similarity 34.61;
Qy	118 -CLKRSRCPPESSGYYQAGTPTERNITYCKKCPGFFSETSSAPC1-KHTNCTSTFGLLRIQ	17.5	Db	66; Mismatches 118; Indels 118; Gaps 118;
Qy	122 RQMRSLKCGPFGVQVASSRAPNGVNLCKACAPGTFSDTSSDVRPHRICSS--ILAI	17.7	Db	66; Alternative names: 75K tumor necrosis factor receptor type 2
Qy	176 KGNATHDNVCS 18.6	17.8	Db	66; Species: Homo sapiens (man)
Qy	178 PGNSTDAVCA 18.8	17.8	Db	66; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
RESULT 2	A35356	17.8	Db	C:Accession: A35356 ; MUID: 90260639 ; PMID: 2160731
				A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
				A:Reference number: A35356 ; MUID: 90260639 ; PMID: 90260639
				A:Accession: A35356 ; MUID: 90260639 ; PMID: 2160731
				A:Status: preliminary

A; Molecule type: mRNA	F; 280-461/Domain: intracellular #status predicted <INT>
A; Residues: 1-461 <SMI>	F; 171-193/Binding site: carbohydrate (Asn) (covalent) #status predicted
A; Cross-references: UNIPROT:P20333; UNIPARC:UPI000002FAE1; GB:M32315; NID:9189185; PIDN:R; Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990	Query Match 14-3%; Score 312; DB 1; Length 461;
A; Title: A second tumor necrosis factor receptor gene product can bind a naturally occur	Best Local Similarity 34.7%; Pred. No. 3.6e-14;
A; Reference number: A36475; MUID:91045931; PMID:2172983	Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
A; Accession: A36475	Qy 8 ALVLVDIEMTQTETLPPK -VLYHDPEGH-----QLLCDKCAPGTYLQKH 53
A; Status: preliminary	Db 9 ALAVGEL -WAAAHLPAQVAFYTAPEPGSTCRIREYYDQTAGMCSCSKCSPGQHAKV 66
A; Molecule type: mRNA	
A; Residues: 1-195 'R', 197-461 <KOH>	
A; Cross-references: UNIPARC:UPI00003475F; GB:M55994; PIDN:AAA36	Qy 54 CTVRKHCYCPDPSYTSWHTSISVQKCBGRLY 113
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)	Db 67 CTKTSDTVDSCEDSTYTLQMNWWFECLSGSRCSSDQVETQACTREONRRICTCPGWYC 126
A; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahn, H.W.; Gentz, R.; Brockhaus, M.	
Cytokine 2, 231-237, 1990	Qy 114 EI-----BPLKHKRSCPPGSGVVAQGTPERNTVCKKCPDGFSEGETSSKAPCIRHTNCS 167
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular,	Db 127 ALSKQEGCRCLCAPLKKCRPGFVAPGTTSDVVKCPADGFTSNTSSDICRHQICN 186
A; Reference number: A48416; MUID:91370650; PMID:1966549	
A; Accession: A48416	
A; Status: preliminary	
A; Molecule type: mRNA; protein	Qy 168 TFGLLIQLQGNATHDNVC 186
A; Residues: 23-461 <DEM>	Db 187 VVAV----PERASMDAVCT 201
A; Cross-references: UNIPARC:UPI00001736B6; GB:S63368; NID:9235649; PIDN:AAB19824.1; PID:R; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.	
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)	
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra	
A; Reference number: A36007; MUID:90349572; PMID:2166946	
A; Accession: A36007	RESULT 3
A; Status: preliminary	B38634
A; Molecule type: mRNA	tumor necrosis factor receptor type 2 precursor - mouse
A; Residues: 1-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HLU>	C;Species: Mus musculus (house mouse)
A; Cross-references: UNIPARC:UPI00001736B6; GB:S63368; NID:9235649; PIDN:AAB19824.1; PID:R; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.	C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)	C;Accession: B38634; A40254; S54816
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra	R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
A; Reference number: A36007; MUID:90349572; PMID:2166946	Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991.
A; Accession: A36007	A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A; Status: preliminary	A;Reference number: A38634; MUID:91187885; PMID:1849278
A; Molecule type: mRNA	A;Accession: B38634
A; Residues: 1-474 <LEW>	A;Molecule type: mRNA
A; Cross-references: UNIPARC:UPI000003B93; GB:M60469; PIDN:9199827; PIDN:R; Chernajovsky, Y.	A;Cross-references: UNIPARC:UPI000003B93; GB:M60469; PIDN:9199827; PIDN:R; Chernajovsky, Y.
A; Status: preliminary	R;Goodwin, R.G.; Anderson, D.; Jezyk, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
A; Molecule type: protein	Mol. Cell. Biol. 11, 3020-3026, 1991.
A; Residues: 27-31 <BNG>	A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A; Cross-references: UNIPARC:UPI00001736E7; UNIPARC:UPI00001736B8; R;Engelmann, H.; Novick, D.; Wallach, D.	A;Reference number: A40254; MUID:91246168; PMID:1645445
A; Status: preliminary	A;Accession: A40254
A; Molecule type: DNA	A;Molecule type: mRNA
A; Residues: 1-474 <GOO>	A;Cross-references: UNIPARC:UPI000003B93; GB:M60469; PIDN:9199827; PIDN:R; Kissborth, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
A; Cross-references: UNIPARC:UPI00001736EA	C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
A; Status: preliminary	C;Keywords: cytokine receptor; transmembrane protein
A; Molecule type: DNA	F; 1-22/Domain: signal sequence #status predicted <SIG>
A; Residues: 1-37 <RES>	F; 23-474/Domain: tumor necrosis factor receptor type 2 #status predicted <MAT>
A; Cross-references: UNIPARC:UPI000006D8; EMBL:X80021; PIDN:CAA56324.1; PI	F; 40-77/Domain: NGF receptor repeat homology <NG1>
A; Status: preliminary	F; 79-120/Domain: NGF receptor repeat homology <NG4>
A; Molecule type: protein	F; 165-203/Domain: NGF receptor repeat homology <NG4>
A; Reference number: 138094	Query Match 14-3%; Score 312; DB 2; Length 474;
A; Accession: 138094	Best Local Similarity 34.3%; Pred. No. 3.7e-14;
A; Status: preliminary	Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;
A; Molecule type: DNA	C;Superfamily: duplication; glycoprotein; receptor; transmembrane protein
A; Residues: 1-37	C;Keywords: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
A; Cross-references: UNIPARC:UPI00001736EA	C;Signal sequence #status predicted <SIG>
A; Status: preliminary	C;Keywords: tumor necrosis factor receptor type 2 #status experimental <MAT>
A; Introns: 26/3	C;Cross-references: GB:TNR1919; OMIM:191191
A; Gene: GDB:TNR2	Qy 5 LCCALVLDLIEWTTQETLPPKU -HYDPEGH-----QLLCDKCAPGTY 49
A; Cross-references: GDB:125914; OMIM:191191	Db 6 LWVALVPELQL -WATGHTVPAQVLTTPKPEPGECQISQEYDRKAQMCCKAQPQGY 63
A; Molecule type: protein	Db 164-201/Domain: NGF receptor repeat homology <NG3>
A; Position: 1p36.2-1p36.2	Qy 262-279/Domain: NGF receptor repeat homology <NG3>
A; Cross-references: GDB:125914; OMIM:191191	F; 120-162/Domain: NGF receptor repeat homology <NG3>
A; Status: preliminary	F; 222-279/Domain: NGF receptor repeat homology <NG3>
A; Molecule type: protein	F; 279-321/Domain: NGF receptor repeat homology <NG3>
A; Position: 1p36.2-1p36.2	Qy 322-379/Domain: NGF receptor repeat homology <NG3>
A; Cross-references: GDB:125914; OMIM:191191	F; 322-379/Domain: NGF receptor repeat homology <NG3>
A; Status: preliminary	Qy 379-431/Domain: NGF receptor repeat homology <NG3>
A; Molecule type: protein	F; 432-484/Domain: NGF receptor repeat homology <NG3>
A; Position: 1p36.2-1p36.2	Qy 432-484/Domain: NGF receptor repeat homology <NG3>
A; Cross-references: GDB:125914; OMIM:191191	F; 484-536/Domain: NGF receptor repeat homology <NG3>
A; Status: preliminary	Qy 501KQHCTVRRRLCVPCKDLSYDXTSHHTSDECVYCPVCKLQLSVRQECDNTHNRCECE 109

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw. model

Run on: May 15, 2006, 18:46:34 ; Search time 115.667 Seconds
(without alignments)

1523.264 Million cell updates/sec

Title: US-09-718-725A-123

Perfect score: 21.9

Sequence: 1 MNKWLCCALLYLIDIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapoff 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP19808:*

2: geneseqP19909:*

3: geneseqP20008:*

4: geneseqP20018:*

5: geneseqP20028:*

6: geneseqP20038:*

7: geneseqP20039:*

8: geneseqP20048:*

9: geneseqP20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Location/Qualifiers
1	21.79	100.0	401	2 AAW38344	AAw38344 Mouse ost	90. .1295
2	21.79	100.0	401	4 AAB80898	AAb80898 Human ost	/tag= a
3	21.79	100.0	401	4 AAY72916	AAy72916 Human ost	/product= "osteoprotegerin"
4	21.79	100.0	401	4 AAB66975	AAb66975 Murine OP	
5	21.79	100.0	401	8 ADM28811	ADM28811 Mouse ost	XX
6	21.79	100.0	401	9 AEB19866	AEB19866 Murine os	PD 26-JUN-1997.
7	21.64	99.3	401	9 AEB19806	AEB19806 Osteoprot	XX
8	20.79	95.4	401	2 AAW38343	AAw38343 Rat osteo	PF 20-DEC-1996;
9	20.79	95.4	401	4 AAB66974	AAb66974 Rat OPG,	XX
10	20.79	95.4	401	8 ADM28809	ADM28809 Rat osteo	PR 22-DEC-1995;
11	20.79	95.4	401	9 AEB19867	AEB19867 Rat osteo	PR 03-SEP-1996;
12	19.00	95.0	401	9 AEB19804	AEB19804 Osteoprot	XX
13	20.61	94.6	380	4 AAB66987	AAB66987 Human OPG	PA (AMGE-) AMGEN INC.
14	20.61	94.6	380	8 ADM28826	ADM28826 Mouse ost	XX
15	19.00	94.6	380	9 AEB19855	AEB19855 Osteoprot	PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
16	20.50	94.1	380	8 ADM28861	ADM28861 Mouse ost	XX
17	19.00	87.2	401	2 AAY05742	AAY05742 Tumour ne	DR WPI ; 1997-334271/31.
18	19.00	87.2	401	2 AAW95030	AAw95030 Tumour ne	DR N-PSDB; AAT96062.
19	19.00	87.2	401	2 AAW83926	AAw83926 Human FTH	XX
20	19.00	87.2	401	3 AAB18715	AAB18715 A human t	PT Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
21	19.00	87.2	401	4 AAB60570	AAB60570 Human TNF	PT involving excessive bone loss, e.g. osteoporosis.
22	19.00	87.2	401	6 AAE36245	AAE36245 Human TRA	XX
23	19.00	87.2	401	6 AAO31135	AAO31135 Human TRA	PS
24	19.00	87.2	401	7 ADD01625	ADD01625 Human ost	CC The present sequence is mouse osteoprotegerin (OPG). Anti-OPG antibodies

can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the cDNA can be used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or prevent bone diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss, bone necrosis and osteopaenia.

SQ Sequence 401 AA:

Query Match 100.0%; Score 2179; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 2.9e-174; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDLIEWTQETLPPKLYHDPETGHQLLCKCAGTLYLKHCTYRKT 60
 Db 1 MNKWLCCALLVLDLIEWTQETLPPKLYHDPETGHQLLCKCAGTLYLKHCTYRKT 60
 Qy 61 LCVPCPDHYSYTDWHTSDECVYCSPVCKELQSVKQECNRTHNRCVCEGRYLEEFCLK 120
 Db 61 LCVPCPDHYSYTDWHTSDECVYCSPVCKELQSVKQECNRTHNRCVCEGRYLEEFCLK 120
 Qy 12.1 HRSCPPGSVVOAGTPERTNTVCKKCPDPGFFGETSSKAPC1KHTNGSTFGHLLIQGNAT 180
 Db 12.1 HRSCPPGSVVOAGTPERTNTVCKKCPDPGFFGETSSKAPC1KHTNGSTFGHLLIQGNAT 180
 Qy 18.1 HDNVCSNREATAOKCGIDVTLCEAFAFPVPTKIPPNWLSVLDSPGTVNAESVERI 240
 Db 18.1 HDNVCSNREATAOKCGIDVTLCEAFAFPVPTKIPPNWLSVLDSPGTVNAESVERI 240
 Qy 24.1 KRRHSSQETFQKLWKHQNDQEMYKIIQDIDCCESSYQRHLGHSLNTTEQIAAME 300
 Db 24.1 KRRHSSQETFQKLWKHQNDQEMYKIIQDIDCCESSYQRHLGHSLNTTEQIAAME 300
 Qy 30.1 SLPGKKSISPEE1ERTRACKSSBQLLKLSLWRKNGDQDTLKGMYALKHLTKSHFPKT 360
 Db 30.1 SLPGKKSISPEE1ERTRACKSSBQLLKLSLWRKNGDQDTLKGMYALKHLTKSHFPKT 360
 Qy 36.1 VTHSLRKMRFLHSFTMRYLFLKPLLEMIGNQYQSYKISCL 401
 Db 36.1 VTHSLRKMRFLHSFTMRYLFLKPLLEMIGNQYQSYKISCL 401
 XX SQ Sequence 401 AA:

RESULT 2
 AAB80898 standard; protein; 401 AA.

XX ID AAB80898
 XX AC AAB80898;
 XX DT 31-MAY-2001 (first entry)
 XX DE Human osteoprotegrin, OPG.
 XX KW Human; anticancer; Antimetastaotic; Osteogenic; lytic bone disease;
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
 KW osteoclast formation inhibition; bone resorption inhibition.
 XX OS Homo sapiens.
 XX PN WO200117543-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-US022606.
 XX PR 03-SEP-1999; 99US-00389545.
 XX PA (AMGE -) AMGEN INC.
 XX SQ Sequence 401 AA:
 Query Match 100.0%; Score 2179; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.9e-174; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MNKWLCCALLVLDLIEWTQETLPPKLYHDPETGHQLLCKCAGTLYLKHCTYRKT 60
 Db 1 MNKWLCCALLVLDLIEWTQETLPPKLYHDPETGHQLLCKCAGTLYLKHCTYRKT 60
 Qy 61 LCVPCPDHYSYTDWHTSDECVYCSPVCKELQSVKQECNRTHNRCVCEGRYLEEFCLK 120
 Db 61 LCVPCPDHYSYTDWHTSDECVYCSPVCKELQSVKQECNRTHNRCVCEGRYLEEFCLK 120
 Qy 121 HRSCPPGSVVOAGTPERTNTVCKKCPDPGFFGETSSKAPC1KHTNGSTFGHLLIQGNAT 180
 Db 121 HRSCPPGSVVOAGTPERTNTVCKKCPDPGFFGETSSKAPC1KHTNGSTFGHLLIQGNAT 180
 Qy 181 HDNVCSNREATAOKCGIDVTLCEAFAFPVPTKIPPNWLSVLDSPGTVNAESVERI 240
 Db 181 HDNVCSNREATAOKCGIDVTLCEAFAFPVPTKIPPNWLSVLDSPGTVNAESVERI 240
 Qy 241 KRRHSSQETFQKLWKHQNDQEMYKIIQDIDCCESSYQRHLGHSLNTTEQIAAME 300
 Db 241 KRRHSSQETFQKLWKHQNDQEMYKIIQDIDCCESSYQRHLGHSLNTTEQIAAME 300
 Qy 301 SLPGKKSISPEE1ERTRACKSSBQLLKLSLWRKNGDQDTLKGMYALKHLTKSHFPKT 360
 Db 301 SLPGKKSISPEE1ERTRACKSSBQLLKLSLWRKNGDQDTLKGMYALKHLTKSHFPKT 360
 Qy 361 VTHSLRKMRFLHSFTMRYLFLKPLLEMIGNQYQSYKISCL 401
 Db 361 VTHSLRKMRFLHSFTMRYLFLKPLLEMIGNQYQSYKISCL 401
 XX SQ Sequence 401 AA:

3.01 SLPGKKSISPDIEBERTKTCKPSEBOLKLKLISIWRKINGDODTLKGLMYALKHLKAYHFPKCT 360
 :
 3.01 SLPGKKSISPEBIRTRKTCKPSEBOLKLKLISIWRKINGDODTLKGLMYALKHLKTSHPKCT 360
 3.61 VTHSLRKTCRPLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
 :
 3.61 VTHSLRKTCRPLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401

SULT 2
-10-510-876-2
Sequence 2, Application US/10510876
Publication No. US20060003928A1
GENERAL INFORMATION:
APPLICANT: Power, Christine
APPLICANT: Plater-Zyberk, Christine
TITLE OF INVENTION: Use of osteoprotogerin for the treatment and/or prevention of fib
TITLE OF INVENTION: disease
FILE REFERENCE: SLII-P01-001
CURRENT APPLICATION NUMBER: US/10/510,876
CURRENT FILING DATE: 2004-10-08
PRIOR APPLICATION NUMBER: EP02100364.5
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 87 6%; Score 1914; DB 9; Length 401;
 Best Local Similarity 86.3%; Pred. No. 2-9-151;
 Matches 25; Mismatches 28; Indels 2; Gaps 2;
 Conservative 25; Mismatches 28;

1 MNKWLCCALLVFLDI-IEWTTQETPPKLYHYDPETGQLLDCAPGTYLKQKCTVRRK 59
 1 MNKWLCCA-LVFLDISIKWTTQETPPKLYHYDPEETSHQLLCDCPPGTYLKQKCTAVRK 59
 60 TICLCPEDSYSTDWSHTSDECYCSFVCKELQTYKQECNRTHNRYCBECEGRTYLEFCL 119
 60 TICLCPEDSYSTDWSHTSDECYCSFVCKELQTYKQECNRTHNRYCBECEGRTYLEFCL 119
 60 TICLCPEDSYSTDWSHTSDECYCSFVCKELQTYKQECNRTHNRYCBECEGRTYLEFCL 119
 120 KHRSCPGLGVLYQAGTPERNTVCKRCPDGFSGIETSSKAPCRKTNCCSUGLILIQKENA 179
 120 KHRSCPGLGVLYQAGTPERNTVCKRCPDGFSSNTESSKAPCRKTNCCSUGLILIQKENA 179
 180 THDNVCSGNRNRATQNGIDVTLCEAFAFRPAPTKIIPWLSVLYDLSGTTKNAESVER 239
 180 THDNVCSGNRNRATQNGIDVTLCEAFAFRPAPTKIIPWLSVLYDLSGTTKNAESVER 239
 240 IKRHSSQEQTQFLKLWKHONRQDENVKIIQIDIDCCESSVQRHIGHANLTTEQRLTLM 299
 240 IKRHSSQEQTQFLKLWKHONRQDENVKIIQIDIDCCESSVQRHIGHANLTTEQRLTLM 299
 300 ESLPGKIKISPDEIERTKTKPSEQKLKLWKRKGNDQDTLIGLMLYALKHLLKAYHFK 359
 300 ESLPGKIKISPDEIERTKTKPSEQKLKLWKRKGNDQDTLIGLMLYALKHLLKAYHFK 359
 360 TVTHSLRKTRFLHSFTMMLYQKPLEMIGNQVOSVKISCL 401
 360 TVTHSLRKTRFLHSFTMMLYQKPLEMIGNQVOSVKISCL 401

SULT 3
 -10- 921-793-52
 Sequence 52, Application US/10921793
 Publication No. US20060039919A1
 GENERAL INFORMATION
 APPLICANT: NYCZ, Jeffrey
 TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
 with Conductive Material
 FIELD OF INVENTION: Orthopaedic Devices

```
FILE REFERENCE: 64118 000087
; CURRENT APPLICATION NUMBER: US/10/921,793
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 52
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
;US-10-921-793-52
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein - protein search, using 3W model

on: May 15, 2006, 19:19:25 ; Search time 92 Seconds
(without alignment)
1821.191 Million cell updates/sec

file: US-09-718-725A-121

effect score: 2185

sequence: 1 MNKWLCCALLVFLDIEWTT.....OKLFLEMIGNQVQSVKISCL 401

string table: BLOSUM62
Gapext 10.0 , Gapext 0.5

searched: 1867559 seqs, 417829326 residues

al number of hits satisfying chosen parameters: 1867569

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

abase : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.per:*

2: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.per:*

3: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.per:*

4: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.per:*

5: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.per:*

6: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.per:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-405-032-121
Sequence 121, Application US/09405032
Publication No. US20030207827A1

GENERAL INFORMATION:

APPLICANT: Amgen Inc.

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehaviland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: United States

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.1, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/405,032

FILING DATE: 24-Sep-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378-CIP2

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-405-032-121

Query Match Score 2185; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1..1e-177;
Matches 401; Mismatches 0; Indels 0; Gaps

Y 1 MNKWLCCALLVFLDIEWTTQETPPKYLHYDPETGROLLDKCAPGTYLKQHCTYRKT 60
D 1 MNKWLCCALLVFLDIEWTTQETPPKYLHYDPETGROLLDKCAPGTYLKQHCTYRKT 60

Db 1 MNKWLCCALLVFLDIEWTTQETPPKYLHYDPETGROLLDKCAPGTYLKQHCTYRKT 60

Qy 1 LCVCPDYSYSTDSWTSDECVYSPVCKELQTVROCNTRHVCBEGRYLELFCLK 12
D 1 LCVCPDYSYSTDSWTSDECVYSPVCKELQTVROCNTRHVCBEGRYLELFCLK 12

Qy 121 HRSCEPGLGVLAQTPERNVTCKRCBDFGSGETSSKAPCRKHTNCSSLGLLIGKNAT 18

1 MNKWLCCALLVFLDIEWTTQETPPKYLHYDPETGROLLDKCAPGTYLKQHCTYRKT 60
2 Sequence 121, APP
3 Sequence 121, APP
4 Sequence 121, APP
5 Sequence 121, APP
6 Sequence 121, APP
7 Sequence 123, APP
8 Sequence 123, APP
9 Sequence 123, APP
10 Sequence 123, APP
11 Sequence 123, APP
12 Sequence 123, APP
13 Sequence 123, APP
14 Sequence 138, APP
15 Sequence 175, APP
16 Sequence 5, Appli
17 Sequence 5, Appli
18 Sequence 5, Appli
19 Sequence 5, Appli
20 Sequence 2, Appli
21 Sequence 2, Appli
22 Sequence 528, APP
23 Sequence 529, APP
24 Sequence 542, APP
25 Sequence 1238, AP
26 Sequence 1239, AP
27 Sequence 1241, AP

1 MNKWLCCALLVFLDIEWTTQETPPKYLHYDPETGROLLDKCAPGTYLKQHCTYRKT 60
2 Sequence 121, APP
3 Sequence 121, APP
4 Sequence 121, APP
5 Sequence 121, APP
6 Sequence 121, APP
7 Sequence 123, APP
8 Sequence 123, APP
9 Sequence 123, APP
10 Sequence 123, APP
11 Sequence 123, APP
12 Sequence 123, APP
13 Sequence 123, APP
14 Sequence 138, APP
15 Sequence 175, APP
16 Sequence 5, Appli
17 Sequence 5, Appli
18 Sequence 5, Appli
19 Sequence 5, Appli
20 Sequence 2, Appli
21 Sequence 2, Appli
22 Sequence 528, APP
23 Sequence 529, APP
24 Sequence 542, APP
25 Sequence 1238, AP
26 Sequence 1239, AP
27 Sequence 1241, AP

Db 121 HRSCPGLGVLOAGTPERNTVKRCPDGFSSGETSSKAPCRKHTNCSSLGILLIQGNAT 180
 Qy 181 HDNVCSGNREATONCGIDVTLCEAEPFAVETKILLPNTLSSLPGTKVNAESEVERI 240
 Db 181 HDNVCSGNREATONCGIDVTLCEAEPFAVETKILLPNTLSSLPGTKVNAESEVERI 240
 Qy 241 KRRHSSQEQTQFQLKLMKHONRDQEMVKIKIODIDCESSVORIGHANLTTEQRLIME 300
 Db 241 KRRHSSQEQTQFQLKLMKHONRDQEMVKIKIODIDCESSVORIGHANLTTEQRLIME 300
 Qy 301 SLPGKKSISPDDELERTRKCKPSBQLKLSSLWRKNGDQTLKGMLYALHLKATHFPKT 360
 Db 301 SLPGKKSISPDDELERTRKCKPSBQLKLSSLWRKNGDQTLKGMLYALHLKATHFPKT 360
 Qy 361 VTHSLRKTRFLHSFTMYRLYOKLFLMIGNOVOSVKSCL 401
 Db 361 VTHSLRKTRFLHSFTMYRLYOKLFLMIGNOVOSVKSCL 401
 Qy 361 VTHSLRKTRFLHSFTMYRLYOKLFLMIGNOVOSVKSCL 401
 Db 361 VTHSLRKTRFLHSFTMYRLYOKLFLMIGNOVOSVKSCL 401

RESULT 2
 US-10-762-159-121
 Sequence 121, Application US/10762159
 GENERAL INFORMATION:
 APPLICANT: Boyle, William J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi.
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 168
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Angen Inc.
 STREET: 1840 Dehavenland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: United States
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/762,159
 FILING DATE: 2004-JAN-20
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/132,985
 FILING DATE: 1998-AUG-12
 APPLICATION NUMBER: 08/771,777
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-378-CIP
 SEQUENCE FOR SEQ ID NO: 121:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 99.6%; Score 2177; DB 6; Length 401;
 Best Local Similarity 99.8%; Pred. No. 5.5e-177;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 HRSCPGLGVLOAGTPERNTVKRCPDGFSSGETSSKAPCRKHTNCSSLGILLIQGNAT 120
 Qy 121 HDNVCSDYTSWHTSDCVCYCSVCKELQTVKQECNRTHNVCCEGRYLEEFLCK 120
 Db 121 HDNVCSDYTSWHTSDCVCYCSVCKELQTVKQECNRTHNVCCEGRYLEEFLCK 120
 Qy 121 MNKWLCCALLVPLDIEWTTQETFPKLYHDPETGRQLLCDKCAPGTYLKQHCTVRKT 60
 Db 121 MNKWLCCALLVPLDIEWTTQETFPKLYHDPETGRQLLCDKCAPGTYLKQHCTVRKT 60
 Qy 121 HRSCPGLGVLOAGTPERNTVKRCPDGFSSGETSSKAPCRKHTNCSSLGILLIQGNAT 180
 Db 121 HRSCPGLGVLOAGTPERNTVKRCPDGFSSGETSSKAPCRKHTNCSSLGILLIQGNAT 180
 Qy 181 HDNVCSGNREATONCGIDVTLCEAEPFAVETKILLPNTLSSLPGTKVNAESEVERI 240
 Db 181 HDNVCSGNREATONCGIDVTLCEAEPFAVETKILLPNTLSSLPGTKVNAESEVERI 240

Scoring table:	BLOSUM62	ALIGMENTS					
Gapop:	10.0	Gapext: 0.5					
Searched:	2166443 seqs, 705528306 residues						
Total number of hits satisfying chosen parameters:	2166443						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	UniProt 05_80.0: 1: uniprot_sprot;* 2: uniprot_trembl;*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
		SUMMARIES					
Result No.	Score	Query	Match	Length	DB	ID	Description
1	2485	100.0	401	1	TR11B_RAT	00727 rattus norvegicus	
2	2093	95.8	401	2	Q6P12_MOUSE	06p112 mus musculus	
3	2019	95.1	401	1	TR11B_HUMAN	008712 mus musculus	
4	1914	87.6	401	2	Q53P6_MOUSE	053p6 homo sapiens	
5	1909	87.4	401	2	Q4F9K2_CHICK	Q4f9k2 gallus gallus	
6	1493	58.5	68.4	402	2	Q6GLN3_XENLA	Q6gln3 xenopus laevis
7	1010	46.2	387	2	Q4SHB7_TETRADON	Q4shb7 tetradon n	
8	571.5	26.2	480	2	Q72ZY4_CHICK	Q72zy4 gallus gallus	
9	553	25.3	146	2	Q72ZY4_CHICK	Q72zy4 gallus gallus	
10	437	20.0	186	2	Q7ZY5_CHICK	Q7zy5 gallus gallus	
11	425.5	19.5	300	1	TNR6B_HUMAN	Q93407 homo sapiens	
12	406.5	18.6	286	2	Q6NW61_BARE	Q6nw61 brachydanio	
13	386.5	17.7	302	2	Q9P0SO_SALF0	Q9p0so salvelinus	
14	382	17.5	285	2	Q90W71_ONCMTY	Q9w71 oncorhynchus	
15	376	17.2	285	2	Q90Y56_ONCMTY	Q9y56 oncorhynchus	
16	344	15.9	637	2	Q5TNY2_BIAR	Q5tny2 brachydanio	
17	325	14.9	561	2	Q4SHB6_TETRADON	Q4shb6 tetradon n	
18	323	14.8	459	2	Q62327_MOUSE	Q62327 mus musculus	
19	322	14.7	474	1	TNR1B_HUMAN	P2119 mus musculus	
20	322	14.7	474	2	Q54SP4_MOUSE	Q545p4 m adult male	
21	320	14.6	461	1	TNR1B_HUMAN	P20333 m tumor nec	
22	320	14.6	461	2	Q3TR46_HUMAN	Q5thj6 homo sapiens	
23	315	14.4	651	2	Q9B8M6_CHICK	Q9b8m6 gallus gallus	
24	312	14.3	461	2	Q6WAB8_RAT	Q6wab8 rattus norvegicus	
25	312	14.3	474	1	TNR1B_RAT	Q8wyp0 rattus norvegicus	
26	312	14.3	474	2	Q5YLPO_RAT	Q17509 homo sapiens	
27	304.5	13.9	655	1	TNR21_HUMAN	TNR21_HUMAN	
28	295.5	13.5	655	1	TNR21_MOUSE	Q543y9 mus musculus	
29	295.5	13.5	655	2	Q54Y9_MOUSE	Q912m6 rattus norvegicus	
30	292	13.4	433	2	Q912M6_RAT	Q4rf28 tetradon n	
31	278	12.7	463	2	Q4rf28_TESTING		

DR	HSSP; P19438; 1NCNP; Ensemble; ENSEMBL; Rattus norvegicus.	RESULT 2	Q6P112_MOUSE PRELIMINARY;	PRY;	401 AA.
DR	RCD; 619802; Trinrf11b.	ID	Q6P112;		
DR	GO; GO:0045779; P:negative regulation of bone resorption; IMP.	AC			
DR	GO; GO:0045671; P:negative regulation of osteoclast different. . . ; TAS.	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DR	InterPro; IPR004588; Death.	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DR	InterPro; IPR011029; DEATH_like.	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DR	InterPro; IPR001368; TNFR_c6.	DB	Tumor necrosis factor receptor superfamily, member 11b (Osteoprotegerin).		
DR	Pfam; PF00531; Death: 1.	DB	(Osteoprotegerin).		
DR	Pfam; PF00020; TNFR_c6; 3.	GN	Name=Infrasub1;		
DR	SMART; SM00005; DEATH; 1.	OS	Mus musculus (Mouse).		
DR	SMART; SM00208; TNFR; 4.	OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Muridae; Murine; Mus.		
DR	PROSITE; P500017; DEATH DOMAIN; FALSE_NEG.	OC			
DR	PROSITE; PS00050; TNFR_NGPR_1; 1.	OX			
DR	PROSITE; PS00050; TNFR_NGPR_2; 2.	OX			
KW	Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.	OX			
FT	CHAIN 1 21	RN	[1]		
FT	CHAIN 22 401	RP	NUCLEOTIDE SEQUENCE.		
FT		RC	TISSUE=Limb;		
FT		RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
FT	REPEAT 24 62	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullhy S.J., Bosak S.A., Mcowan P.J., McKernan K.J., Malek J.A., Gamarra P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinberg J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT and mouse cDNA sequences"; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
FT	REPEAT 65 105	RA			
FT	REPEAT 107 142	RA			
FT	REPEAT 145 185	RA			
FT	DOMAIN 198 269	RA			
FT	DOMAIN 270 365	RA			
FT	SITE 400 400	RA			
FT	CARBONYD 98 98	RA			
FT	CARBONYD 165 165	RA			
FT	CARBONYD 178 178	RA			
FT	CARBONYD 289 289	RA			
FT	DISULFID 41 54	RA			
FT	DISULFID 44 62	RA			
FT	DISULFID 65 80	RA			
FT	DISULFID 83 97	RA			
FT	DISULFID 87 105	RA			
FT	DISULFID 107 118	RA			
FT	DISULFID 124 142	RA			
FT	DISULFID 145 160	RA			
FT	DISULFID 166 185	RA			
SQ	SEQUENCE 401 AA; 46192 MW; FECGA31F1D4E573A CRC64;	RA			
Query	Query Match 100.0% ; Score 2185; DB 1; Length 401; Best Local Similarity 100.0% ; Pred. No. 7e-151; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RN	NUCLEOTIDE SEQUENCE.		
Query	1 MNKWLCCALLVLDIETWTTQETFPKLYHDPETRQLLCKCAGTYLKQHCTVTRKT 60	RC	TISSUE=Limb;		
Db	1 MNKWLCCALLVLDIETWTTQETFPKLYHDPETRQLLCKCAGTYLKQHCTVTRKT 60	RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
Query	61 LCVPCPDPSYDSDWTSDECYCSPVCKELQTVKQECNRTINVCCEGRYLELFCLK 120	DR	EMBL: BC049782; AAH9782.1; - mRNA.		
Db	61 LCVPCPDPSYDSDWTSDECYCSPVCKELQTVKQECNRTINVCCEGRYLELFCLK 120	DR	GO: GO:0005578; C: extracellular space; TAS.		
Query	61 HRSCPPGIGVLOGATPPTNTVCKRCPDGFSSGETSSAKAPCRKHTNGSSLGILLIQGNAT 180	DR	GO: GO:0042489; P:negative regulation of odontogenesis (sensu . . .); IDA.		
Db	121 HRSCPPGIGVLOGATPPTNTVCKRCPDGFSSGETSSAKAPCRKHTNGSSLGILLIQGNAT 180	DR	INTERPRO; IPR00488; Death.		
Query	181 HDNVCSNREATAQNCIDVTLCBEAFFRAVTPKLIQVTKVNAESEVERI 240	DR	PROSITE; PS00617; TNFR_NGFR_1; 1.		
Db	181 HDNVCSNREATAQNCIDVTLCBEAFFRAVTPKLIQVTKVNAESEVERI 240	DR	PROSITE; PS00531; Death; 1.		
Query	241 KRRHSSQEQTFQQLKMHQNDQEMVKKIQTIDLCESSVQRHGHANLTTEQLRILME 300	DR	PROSITE; PS00622; TNFR_NGFR_2; 2.		
Db	241 KRRHSSQEQTFQQLKMHQNDQEMVKKIQTIDLCESSVQRHGHANLTTEQLRILME 300	DR	PROSITE; PS00531; Death; 1.		
Query	301 SLPGKKISPDDETRTKCKPQEQLKLISWRKGQDQTLKGMLYAKHLKAYTHFPKT 360	DR	SEQUENCE 401 AA; 45965 MW; 7C70708E52EB46BA0E CRC64;		
Db	301 SLPGKKISPDDETRTKCKPQEQLKLISWRKGQDQTLKGMLYAKHLKAYTHFPKT 360	DR	Query Match 95.8%; Score 2093; DB 2; Length 401; Best Local Similarity 95.8%; Pred. No. 3.6e-144; Matches 381; Conservative 10; Mismatches 10; Indels 0; Gaps 0;		
Query	361 VTHSLRKTRTIRFLHSFTMVRFLQKFLIEMIGQYQSYTKSCL 401	DR	1 MNKWLCCALLVLDIETWTTQETFPKLYHDPETRQLLCKCAGTYLKQHCTVTRKT 60		
Db	361 VTHSLRKTRTIRFLHSFTMVRFLQKFLIEMIGQYQSYTKSCL 401	DR	61 LCVPCPDPSYDSDWTSDECYCSPVCKELQTVKQECNRTINVCCEGRYLELFCLK 120		

Protein - protein search, using SW model									
On: May 15, 2006, 18:53:14 ; Search time 21 Seconds (without alignments)		1837.282 Million cell updates/sec							
Table: US-09-718-725A-121					Effect score: 2185 1 MNKMLCCALLVFLDIEWTT.....QRFLFLEMIGNQVQSVKISCL 401				
String table: BLOSUM62 Gapop 10.0 , Gapext 0.5					Scored: 283416 seqs, 96216763 residues				
Number of hits satisfying chosen parameters: 283416					Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	323	14.8	459	2	Gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)				
2	322	14.7	474	2	C;Species: Mus musculus (house mouse)				
3	320	14.6	461	1	C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004				
4	313	14.3	651	1	C;Accession: I48854				
5	272	12.4	305	2	R;Powell, B.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.				
6	263	12.0	277	2	Mamm. Genome 5, 726-727, 1994				
7	2241	11.0	325	2	A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.				
8	225.5	10.8	435	2	A;Reference number: I48854; PMID:95178848; PMID:1773884				
9	217	9.9	326	1	A;Status: preliminary; translated from GB/EMBL/DDBJ				
10	211.5	9.7	349	2	A;Molecule type: mRNA				
11	210.5	9.6	349	2	A;Cross-references: UNIPROT:Q62327; UNIPARC:UPI0000007066; EMBL:X76401; NID:9				
12	207	9.5	348	2	C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology				
13	186	8.5	335	2	F;151-188/Domain: NGF receptor repeat homology				
14	180.5	8.3	314	2	Query Match 14.8%; Score 323; DB 2; Length 459;				
15	179	8.2	256	2	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
16	179	8.2	416	1	Matches 68; Conservative				
17	177	8.1	427	1	Query Match 14.8%; Score 323; DB 2; Length 459;				
18	173	7.9	425	1	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
19	167	7.6	455	1	Matches 68; Conservative				
20	167	7.6	455	1	Query Match 14.8%; Score 323; DB 2; Length 459;				
21	160	7.3	454	1	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
22	158.5	7.3	271	2	Query Match 14.8%; Score 323; DB 2; Length 459;				
23	158.5	7.3	461	2	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
24	156	7.1	461	2	Query Match 14.8%; Score 323; DB 2; Length 459;				
25	152	7.0	277	2	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
26	151	6.9	595	2	Query Match 14.8%; Score 323; DB 2; Length 459;				
27	147.5	6.8	272	2	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				
28	145.5	6.7	324	2	Query Match 14.8%; Score 323; DB 2; Length 459;				
29	144	6.6	327	2	Best Local Similarity 35.6%; Pred. No. 1.3e-15; Mismatches 80; Indels 26; Gaps				

A;Cross-references: UNIPROT:P25119; UNIPARC:UPI0000003893; GB:M60469; NID:9199827; PIDN:R; Goodwin, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3029, 1991
 A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A;Accession: A40254
 A;Molecule type: mRNA
 A;Residues: 1-474 <GO>
 A;Cross-references: UNIPARC:UPI0000003893; GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:R; Kisselburgh, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
 A;Keywords: cytokine receptor; transmembrane protein
 E;1-22/Domain: signal sequence #status Predicted <SIG>
 E;23-474/Product: tumor necrosis factor receptor type 2 #status Predicted <MAT>
 E;40-77/Domain: NGF receptor repeat homology <NG1>
 E;79-120/Domain: NGF receptor repeat homology <NG2>
 E;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 14.7%: Score 322; DB 2; Length 474;
 Best Local Similarity 35.1%; Pred. No. 1.6e-15;
 Matches 72; Conservative 20; Mismatches 83; Indels 30; Gaps 6;

Qy 4 WLCCALLVFLDIEWTQETFPKYL-HYDDETG-----RQLIDDKCAPGT 48
 Db 7 WVA--ELQWLAWGTVPAQVVLTTPYKPEPGYECQISQEYVYDRKAQMCCKAQPQGQ 62

Qy 49 YLKQHCTVTRKTLCKVCPDYSYTDMSWTSDECVYCSPEVQKRCPDGFSGTSSKKAPCR 108
 Db 63 YTKHFCNKTSDTVCADCEASMYTQWVNQFRTLSCSSSCTDQVEFRACTQKQNRVCAE 122

Qy 109 EGRYLELF-----CLKHRSCKCPGIGVQAGTPERBNTYCKRCPDGFSGTSSKKAPCR 161
 Db 123 AGRYCAKTHSSCSCROQMLRSKCGPFGFGRAPNVLCKACAPGTFSDTTSTDVCR 182

Qy 162 KHTNCSSGLLIIQKNAHTDNVCS 186
 Db 183 PHRICLAI1---PGNASTDAVCA 203

RESULT 3
 A35356 tumor necrosis factor receptor 2 precursor [validated] - human
 N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
 C;Species: Homo sapiens (man)
 C;Accession: 10-Sep-1999 # sequence-revision 10-Sep-1999 # text-change 09-Jul-2004
 C;Accession: A35356; A36415; A48416; A36007; A23666; B35010; I38094
 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.R.
 Science 248, 1019-1023, 1990
 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A;Reference number: A35356; MUID:90260639; PMID:2160731
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-461 <SMN>
 A;Cross-references: UNIPROT:P20333; UNIPARC:UPI00002FAE1; GB:M32315; NID:9189185; PIDN:R; Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A;Reference number: A36475; MUID:91045991; PMID:2172983
 A;Status: preliminary
 A;Accession: A36475
 A;Molecule type: mRNA
 A;Residues: 1-195, 'R', 197-461 <KOH>
 A;Cross-references: UNIPARC:UPI00003475F; GB:M55994; NID:9339757; PIDN:AAA36 R; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Laih, H.W.; Gentz, R.; Brockhaus, M.

Qy 8 ALLVFLDIIENTTQETFPK--YIHYDPETG-----ROLLCDKCAPGTYLKQH 53
 Db 9 ALAVGIEL--WAAAALPAQVAFYTAPEGSGTCTREYYDQTAQMCSCSKCSPGGHAKVF 66

Qy 54 CTVRRTKTLCVCPDYSYTDWHTSDBCVYCSPVCKELQTVKQECNRTHNRVCECEBGRYL 113

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
protein - protein search, using sw model
on: May 15, 2006, 18:46:34 ; Search time 115.667 seconds
(without alignments)
1523.264 Million cell updates/sec
Title: US-09-718-725A-121
Accession: 2155
Score: 1 MNKWLCCALLVFLDIIWTT.....QKLFLEMIGNQVSVKISCL 401
Sequence: 1 MNKWLCCALLVFLDIIWTT.....QKLFLEMIGNQVSVKISCL 401
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Number of hits satisfying chosen parameters: 2443163
Human alb 25 Adf16158 Human alb
Human alb 26 Adf16153 Human alb
Human alb 27 Adf16151 Human alb
Human alb 28 Adf15231 Human alb
Human alb 29 Adf16152 Human alb
Human alb 30 Adf16154 Human alb
Human alb 31 Adf16155 Human alb
Human alb 32 Adf16156 Human alb
Human alb 33 Adf15230 Human alb
Human alb 34 Adf15244 Human alb
Human alb 35 Adf16157 Human TRB
Human alb 36 Adk82154 Human TRB
Human TRB 37 Ady34172 Human TRB
Human TRB 38 Aea27557 Human TRB
Human TRB 39 Aea55153 Human TRB
Human TRB 40 Aeb19868 Human TRB
Human TRB 41 Adf15016 Human TRB
Human TRB 42 Adf15030 Human TRB
Human TRB 43 Aar9925 Full length
Human TRB 44 Aaw5339 Human TRB
Human TRB 45 Aav8822 Human TRB

Accession :	GeneSeq_2.1:	Score :	Score :	Score :
	1: geneseqp1990s:*	1	XX	XX
	2: geneseqp1990s:*	2	AC	AAW38343;
	3: geneseqp2000s:*	3	AC	XX
	4: geneseqp2010s:*	4	DT	XX
	5: geneseqp2002s:*	5	DT	20-APR-1998 (first entry)
	6: geneseqp2003sag:*	6	XX	XX
	7: geneseqp2003sb:*	7	XX	Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
	8: geneseqp2004s:*	8	XX	recombinant production; transgenic animal; treatment; prevention;
	9: geneseqp2005s:*	9	XX	antisense oligonucleotide; probe; detection; screening; bone disease;
				osteoporosis; Paget's disease; hypercalcemia; hyperparathyroidism;
				rheumatoid arthritis; osteomyelitis; osteolytic metastasis;
				periodontal bone loss; bone necrosis; osteopaenia.
				XX

SUMMARIES						
Result	Query Score	Match Length	DB ID	Description		
1	2185	100.0	401 2 AAW38243	Aaw38243 Rat osteo	XX	DE19654610-A1.
2	2185	100.0	401 4 AAB66974	Aab66974 Rat OPG.	XX	
3	2185	100.0	401 8 ADM28809	Adm28809 Rat osteo	XX	
4	2185	100.0	401 9 AEB19867	Aeb19867 Rat osteo	XX	22-DEC-1995; 95US-00577788.
5	2177	99.6	401 9 AEB19804	Aeb19804 Osteoprot	XX	03-SEP-1996; 96US-00706945.
6	2079	95.1	401 2 AAW38244	Aaw38244 Mouse ost	XX	
7	2079	95.1	401 4 AAB80598	Aab80598 Human ost	XX	(AMGE-) AMGEN INC.
8	2079	95.1	401 4 AAY72916	Aay72916 Human ost	PT	Boyle WJ, Lacey DL, Calzone FJ, Chang M;
9	2079	95.1	401 4 AAB66975	Aab66975 Murine OP	XX	
10	2079	95.1	401 8 ADM28811	Adm28811 Mouse ost	DR	WPI; 1997-334271/31.
11	2079	95.1	401 9 AEB19866	Aeb19866 Murine os	DR	N-PSDB; AAI96061.
12	2064	94.5	401 9 AEB19806	Aeb19806 Osteoprot	XX	
13	1985	89.9	380 4 AAB66987	Aab66987 Human OPG	PT	Nucleic acid encoding osteoprotegerin - useful for treatment of diseases involving excessive bone loss, e.g. osteoporosis.
14	1965	89.9	380 8 ADM28826	Adm28826 Mouse ost	PT	
15	1965	89.9	380 9 AEB19855	Aeb19855 Osteoprot	XX	
16	1960	89.7	380 8 ADM28861	Adm28861 Mouse ost	PS	Claim 23; Page 102-104; 182pp; German.
17	1914	87.6	401 2 AAY05742	Aay05742 Tumour ne	XX	
18	1914	87.6	401 2 AAW95330	Aaw95330 Tumour ne	CC	The present sequence is rat osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification
19	1914	87.6	401 2 AAW83926	Aaw83926 Human FTH	CC	materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the cDNA can be
20	1914	87.6	401 3 AAB618715	Aab618715 A human t	CC	
21	1914	87.6	401 4 AAB610570	Aab610570 Human TNF	CC	
22	1914	87.6	401 6 AAE36245	Aae36245 Human TRA	CC	
23	1914	87.6	401 7 AAO31135	Aao31135 Human TRA	CC	
24	1914	87.6	401 7 ADD01625	Add01625 Human ost	CC	

CC CDNA libraries for related sequences. OPG can be used to treat or prevent
 CC bone diseases, specifically **excessive** bone loss, e.g. osteoporosis,
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
 CC bone necrosis and osteopaenia

XX Sequence 401 AA;

Query Match 100.0%; Score 2185; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 6.8e-183; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLFIDIDWTTQBTTPPKLYHDPETGRQLLCDKCA9TGYLKQHCTYVTRKT 60
 Db 1 MNKWLCCALLVLFIDIDWTTQBTTPPKLYHDPETGRQLLCDKCA9TGYLKQHCTYVTRKT 60

Qy 61 LCVPCPDYSYTDSWHTSDECYVCSPKCKELQTVKQECNRTHANVCBEGYLELEFCLK 120
 Db 61 LCVPCPDYSYTDSWHTSDECYVCSPKCKELQTVKQECNRTHANVCBEGYLELEFCLK 120

Qy 121 HRSCPPGIGVLAQTPERINTVCKRCPDGFSSGETSSKAPCRKHTNCSSLGHLIQRGNAT 180
 Db 121 HRSCPPGIGVLAQTPERINTVCKRCPDGFSSGETSSKAPCRKHTNCSSLGHLIQRGNAT 180

Qy 181 HDNVCSGNREATAQNCGIDVTLCBEEAFAVPTKILIPNWLSVYLVDSLPGTKVNAESVERI 240
 Db 181 HDNVCSGNREATAQNCGIDVTLCBEEAFAVPTKILIPNWLSVYLVDSLPGTKVNAESVERI 240

Qy 241 KRRHSSDQTFOKLWKRHONDQEMWYKTIQDIDCSESSVORHIGHANLTTEQRILME 300
 Db 241 KRRHSSQDEQTFOKLWKRHONDQEMWYKTIQDIDCSESSVORHIGHANLTTEQRILME 300

Qy 301 SLPGKKSISPDDEBERTTRCKCKPSBQLLKLSLWRKNGDQDTLKGMYALXHLKAYTHFPT 360
 Db 301 SLPGKKSISPDDEBERTTRCKCKPSBQLLKLSLWRKNGDQDTLKGMYALXHLKAYTHFPT 360

Qy 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401
 Db 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401

RESULT 2
 AAB66574 ID AAB66974 standard; protein; 401 AA.
 XX AC AAB66574;
 XX DT 19-APR-2001 (first entry)
 XX DB Rat OPG.
 XX

Bone loss; **osteoprotegerin**; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; septic shock; systemic lupus erythematosus; graft-versus-host disease; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarct; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.

KW XX PD 18-JAN-2001.
 XX PP 07-JUL-2000; 2000WO-US018657.
 XX PR 09-JUL-1999; 99US-00350670.
 XX PR 09-DEC-1999; 99US-00457647.
 XX PA (AMGE-) AMGEN INC.
 XX PT Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WO200103719-A2.
 XX OS Rattus sp.
 XX PN XX
 XX PD 18-JAN-2001.
 XX PP 07-JUL-2000; 2000WO-US018657.
 XX PR 09-JUL-1999; 99US-00350670.
 XX PR 09-DEC-1999; 99US-00457647.
 XX PA (AMGE-) AMGEN INC.
 XX PT Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX Disclosure; Fig 2; 316pp; English.
 XX PS
 CC The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering purified and isolated osteoprotegerin (OPG) protein (AAFS7836-AAF7838 and AAF6694-AAF6697-Alpha CC in conjunction with other substances such as tumour necrosis factor-Alpha (TNF-Alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GvHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock.

XX Sequence 401 AA;

Qy 1 MNKWLCCALLVLFIDIDWTTQBTTPPKLYHDPETGRQLLCDKCA9TGYLKQHCTYVTRKT 60
 Db 1 MNKWLCCALLVLFIDIDWTTQBTTPPKLYHDPETGRQLLCDKCA9TGYLKQHCTYVTRKT 60

Qy 61 LCVPCPDYSYTDSWHTSDECYVCSPKCKELQTVKQECNRTHANVCBEGYLELEFCLK 120
 Db 61 LCVPCPDYSYTDSWHTSDECYVCSPKCKELQTVKQECNRTHANVCBEGYLELEFCLK 120

Qy 121 HRSCPPGIGVLAQTPERINTVCKRCPDGFSSGETSSKAPCRKHTNCSSLGHLIQRGNAT 180
 Db 121 HRSCPPGIGVLAQTPERINTVCKRCPDGFSSGETSSKAPCRKHTNCSSLGHLIQRGNAT 180

Qy 181 HDNVCSGNREATAQNCGIDVTLCBEEAFAVPTKILIPNWLSVYLVDSLPGTKVNAESVERI 240
 Db 181 HDNVCSGNREATAQNCGIDVTLCBEEAFAVPTKILIPNWLSVYLVDSLPGTKVNAESVERI 240

Qy 241 KRRHSSDQTFOKLWKRHONDQEMWYKTIQDIDCSESSVORHIGHANLTTEQRILME 300
 Db 241 KRRHSSQDEQTFOKLWKRHONDQEMWYKTIQDIDCSESSVORHIGHANLTTEQRILME 300

Qy 301 SLPGKKSISPDDEBERTTRCKCKPSBQLLKLSLWRKNGDQDTLKGMYALXHLKAYTHFPT 360
 Db 301 SLPGKKSISPDDEBERTTRCKCKPSBQLLKLSLWRKNGDQDTLKGMYALXHLKAYTHFPT 360

Qy 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401
 Db 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401

Qy 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401
 Db 361 VTHSLRKTRFLHSTMYRLYQKFLLEMIGNOVSYKISCL 401

RESULT 3
 ADM28809 ID ADM28809 standard; protein; 401 AA.
 XX AC ADM28809;
 XX DT 20-MAY-2004 (first entry)
 XX DB Rat osteoprotegerin, OPG.